*4

GenCore version 5.1.6 Copyright (c) 1993 - 2005 Compugen Ltd. OM protein - protein search, using sw model

Run on:

April 1, 2005, 13:24:31 ; Search time 138.696 Seconds (without alignments) 81.226 Million cell updates/sec

1 XXXXXWSXXXXCSXXCGXXXXX 22 US-09-462-909D-9 59 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

1612378 seqs, 512079187 residues Searched:

1612378 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

UniProt 03:*
1: uniprot sprot:*
2: uniprot_trembl:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4	negribrion	Q69hl7 ciona intes	Q86pg3 cryptospori				Q966k7 caenorhabdi	Q8bve5 m mus muscu	Q6zpq8 mus musculu	Q22580 caenorhabdi		Q6pck8 xenopus lae			แนยก	Q7qc32 anopheles g		Q7tt33 mus musculu	homo	P07996 homo sapien	1 mus m	Q718a3 rattus norv	Q80yg1 mus musculu	Q8cgb2 mus musculu	Q9c0i4 homo sapien	Q6p4u0 mus musculu	Q8cg65 mus musculu	Q700k0 rattus norv	043982 cryptospori	Q8mxy6 cryptospori	_	٥,
ć.	77	Q69HL7	Q86PQ3	Q7KYY3	076510	Q69HT6	Q966K7	QBBVES	Q6ZPQ8	Q22580	SM5A_MOUSE	Q6PCK8	Q6UY12	SM5B_HUMAN	SM5B_MOUSE	Q7QC32	Оввирз	Q7TT33	Q6DD89	TSP1_HUMAN	TSP1_MOUSE	Q71SA3	Q80YQ1	Q8CGB2	Q9C014	Q6P4U0	Q8CG65	Q700K0	043982	Q8MXY6	Q9GZ21	Q9GZ22
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Q9gz23 cryptospori Q7jn23 cryptospori	Q24927 eimeria ten Q8qfvl xenopus lae	Q95822 drosophila Q8t988 drosophila	P98060 caenorhabdi O02029 drosophila		Obzgyb mus musculu Q7krf4 drosophila	Q19284 caenorhabdi	Q86pq8 cryptospori	
Q9GZ23 Q7JN23	Q24927 Q8QFV1	Q95S22 Q8T988	TOH2 CAEEL 002029	090746	Q62Q96 Q7KRF4	Q19284	Q86PQ8	Q23832
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ALIGNMENTS

PRELIMINARY;	OCT-2004 (TrEMBLrel. 28, Created) OCT-2004 (TrEMBLrel. 28, Last sequence update) OCT-2004 (TrEMBLrel. 28, Last annotation update)	(Fragment).	Bukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona; phiphysachis: Cinnidae, Ciona	NCBI_TaxID=7719;	[1] SPOTENCE PROM N &		Terajima D., Yamada S., Uchino R., Ikawa S., Ikeda M., Shida K., Arai Y., Wang H.G., Satoh N., Satake M.,	ne	in hemocytes of Ciona intestinalis, three of which may be involved in	cnaracceristic cell-cell communication."; DNA Res. 10:203-212(2003).	EMBL; AY261898; AAP91764.1;	0	errro; irrooiz83; Alirgn_vs/lpxi. errro; irroo0345; CvtC heme BS.	IPR000884; TSP1.		PF00188; SCP; 1.	F-00090;	NTS; PR00837; VSTPXLIKE.	Dom; PD000542; Allrgn_V5/Tpx1; 1.	SM00198; SCP;	SMOUZU9; TS E; PS01009;	PS01010;	PS00190; CYTOCH	SITE; PS50092; TSP1; 5.		JENCE 504 AA; 55337 MW; 305F43A92B850F29 CRC64;	69.5%; Score 41;	ocal Similarity 50.0%; Pred. No. 7.1; s 6; Conservative 0; Mismatches 6; Indels 0; Gaps	
LT 1 L7 Q69HL7 Q69HL7;	25-0CT-2004 25-0CT-2004 25-0CT-2004	HrTT-1-like Ciona intest	Eukaryota;	NCBI_TaxID=	[1] SECTIENCE FE	MEDLINE=230	Terajima D.,	"Identificat	in hemocytes	DNA Res. 10	EMBL; AY2618	GO; GO:0005	InterPro; IN		InterPro, IN	Pfam; PF0018	PRINTS: PROC	PRINTS; PRO	ProDom; PD0(PROSITE; PSO			PROSITE; PS: NON TER	NON TER	SEQUENCE		Best Local Simi Matches 6;	
RESULT Q69HL7 ID Q AC Q	555	OB OS	85	38	22 G	RX	8 8	RT	RT	R.	DR	R I	2 2	D.	DR.	8 E	<u> </u>	DR	DR	<u> </u>	žä	DR	<u>ظ</u> ا	Y F	FT	S	ğ	Be. Mat	

477 WSAWSACSTSCG 488 6 wsxxxxcsxxcg 17 ò 유

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PRELIMINARY; RESULT 2 Q86PQ3 ID Q86PQ3

PRT; 3869 AA.

Gaps

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[1] SEQUENCE FROM N.A. SEQUENCE FROM N.A. MEDILINE-23047825; PubMed=14686582; Exama S., Ikeda M., Shida K., Terajima D., Yamada S., Uchino R., Ikawa S., Ikeda M.; Arai Y., Wang H.G., Satoh N., Satake M.; "Identification and sequence of seventy-nine new transcripts expressed "Identification and sequence of seventy-nine new transcripts expressed in hemocytes of Ciona intestinalis, three of which may be involved in in hemocytes of Ciona intestinalis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  25-OCT-2004 (TrEMBLrel. 28, Created)
25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
Hemicentin-like (Fragment)
Ciona intestinalise (Bragment)
Eukaryota; Metazos; Chordata; Urochordata; Ascidiacea; Enterogona; Phlebobranchia; Cionidae; Ciona.
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                                                                                                                                             Length 59;
                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cryptosporidium parvum.
Bukaryota; Alveolata; Apicomplexa; Coccidia; Eimeriida;
Cryptosporidiidae; Cryptosporidium.
NCBI_TaxID=5807;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        238 238
238 AA; 26307 MW; 28242DE88F62C5A2 CRC64;
                                                                                               C6409E62332708A4 CRC64;
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01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-NAR-2004 (TrEMBLrel. 26, Last annotation update)
Thrombospondin-related adhesive protein (Fragment).
                                                                                                                                               Score 40; DB 2;
Pred. No. 1.8;
0; Mismatches
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PRINTS; PR01705; TSP1REPEAT.
PROSITE; PS50092; TSP1; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
                                                                                                                                                                                                                                                          6 WSXXXXCSXXCG 17
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                                                                                                                                                               Query Match
Best Local Similarity
Matches 6; Conservat
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"Cryptosporidium parvum genes containing thrombospondin type 1
I "Cryptosporidium parvum genes containing thrombospondin type 1
I domains."

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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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MEDLINE=22326344; PubMed=12438378;
DOI=10.1128/IAI.70.12.6987-6995.2002;
Deng M., Templeton T.J., London N.R., Bauer C., Schroeder A.A.,
Abrahamsen M.S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 41; DB 2; Length 3869;
Pred. No. 40;
0; Mismatches 6; Indels
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Dimitry J.M., Sheibani N., Finn M., Boak B.M., Paul L.L.,
Dimitry J.M., Sheibani N., Finn M., Boak B.M., Paul L.L.,
Brazier W.A., GUL.1994) to the EMBL/GenBank/DDBJ databases.
EMBL, U12471; AAA21127.1; -.
EMBL, U12471; AAA21127.1; -.
ELEPTO: IPRO00884; TSP1.
InterPro: IPRO00884; TSP1.
Figam; PF00090; TSP_1: 1.
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SIGNAL 6 25 SOCUENCE 3869 AA; 429514 MW; 1F4851B7B0787BB7 CRC64;
                                                                                                                               Cryptosporidium parvum.

Bukaryota, Alvelata, Apicomplexa, Coccidia, Eimeriida, Cryptosporidiidae, Cryptosporidium.

WCBI_TaxID=5807;
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                                                                       01-JUN-2003 (TrEMBLrel. 24, Last sequence update) 01-MAR-2004 (TrEMBLrel. 26, Last annotation update) TSP1 domain-containing protein TSP2 precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PROSITE; PS00198; 4FEAS FERREDOXIN; UNKNOWN 3. PROSITE; PS000108; 4LDEHYDE_DEHYDR_CYS; UNKNOWN_1.PROSITE; PS0092; TSP1; 10.
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Best Local Similarity 50.0%;
Matches 6; Conservative
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                                                          01-JUN-2003 (TrEMBLrel. 24, 01-JUN-2003 (TrEMBLrel. 24, 01-MAR-2004 (TrEMBLrel. 26,
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RESULT 3

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Gaps

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WormBase; WBGene00017471; F14H12.3.
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Bukaryota, Metazoa, Nematoda, Chromadorea, Rhabditida, Rhabditoidea,
Rhabditidae, Peloderinae, Caenorhabditis.
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                                                                                                                      Score 40; DB 2; Length 238;
Pred. No. 5.8;
0; Mismatches 6; Indels
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Submitted (SEP-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; AC006630; AAK68325.1; -.
HSSP; P07996; 1LSL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=Bristol N2;
Nelson J., Gattung S., R Wilson.;
"The sequence of C. elegans cosmid F14H12.";
Submitted (MAR-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Waterston R.H.;
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases
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                                                                                               7C40DAD7D7C57932 CRC64;
                                                                                                                                                                                                                                                                         01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Hypothetical protein F14H12.3.
                                                                                                                                                                                                                                                      257 AA.
characteristic cell-cell communication.";
DNA Res. 10:203-212(2003).
EMBL; AY261829; AAP91695.1; -.
InterPro; IPR000884; TSP1.
Pfam; PF00090; TSP 1; 4.
SMART; SM00209; TSP 1; 4.
                                                                                                                                                                                                                                                       PRT;
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MEDLINE=99069613; PubMed=9851916;
                                                                                              238 AA; 25294 MW;
                                                                                                                      67.8%;
50.0%;
                                                                                                         Guery Match
Best Local Similarity 50.0.
Best Conservative
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Waterston R.;
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SEQUENCE FROM N.A.
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SEQUENCE
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01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-JM-2003 (TrEMBLrel. 24, Last annotation update)
Mus musculus adult male adrenal gland cDNA, RIKEN full-length enriched
library, clone:7930442016 product:sema domain, seven thrombospondin
repeats (type 1 and type 1-like), transmembrane domain (TM) and short
cytoplasmic domain, (semaphorin) 5B, full insert sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       the RIKEN Genome Exploration Research Group Phase I & II Team; "Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs."; Nature 420:563-573(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
STRANTE-CSPEL(AG) TISSUE=Adrenal gland;
MEDLINE-20499374; PubMed=11042159; DOI=10.1101/gr.145100;
Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
Komno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new genes.";
Genome Res. 10:1617-1630(2000).
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STRAIN=CS7BL/60; INSSUE=Adrenal gland;
MEDLINE=99279273; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
Carninoi P., Hayashizaki Y.;
"High-efficiency full-length cDNA cloning.";
Meth. Enzymol. 303:19-44(1999).
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STRAIN=C57BL/6J; TISSUE=Adrenal gland;
MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
MEDLINE=20530913; PubMed=11076861; Moi=10.1101/gr.152600;
Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P., Konno H., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itoh M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      rtroguezzo...
Mus muscula (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RIKEN FANTOM Consortium; "Functional annotation of a full-length mouse cDNA collection."; Nature 409:685-690(2001).
                                                                                                                                                                                                                                            ;
0
                                                                                                                                                                                                    Length 257;
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STRAIN=C57BL/6J; TISSUE-Adrenal gland;
MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
                                                                                                                                                               9B052A0D07F2BEFF CRC64;
                                                                                                                                                                                                        DB 2;
                                                                                                                                                                                                    Score 40; DB 2
Pred. No. 6.2;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                            478 AA.
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STRAIN=CS7BL/6J; TISSUE=Adrenal gland;
The FANTOM Consortium,
                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
WormPep; F14H12.3; CE07063.
InterPro; IRR00884; TSP1.
InterPro; IPR008085; TSP1.
Pfam; PR00090; TSP 1; 3.
PRINTS; PR01705; TSP1REPEAT.
SMART; SM00209; TSP1; 3.
PROSITE; PSS0092; TSP1; 3.
Hypothetical protein.
SEQUENCE 257 AA; 26512 MW; 9
                                                                                                                                                                                                      67.8%;
50.0%;
                                                                                                                                                                                                                                                                                                                         145 WSSWSACSVTCG 156
                                                                                                                                                                                                                                            6; Conservative
                                                                                                                                                                                                                                                                                    6 WSXXXXCSXXCG 17
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                                                                                                                                                                                                    Query Match
Best Local Similarity
Matches 6; Conserv
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م مان محاله

Gape

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6; Indels

Length 632;

us-09-462-909d-9.rup

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01-000'-1996 (TrEMBLrel. 01, Created)
01-000'-1996 (TrEMBLrel. 20, Last sequence update)
01-MAR-2002 (TrEMBLrel. 26, Last annotation update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Hypothetical protein T19D2.1.
Name=T19D2.1; ORFNames=T19D2.1;
Caenorhabditis elegans
Enkaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Genome sequence of the nematode C. elegans: a platform for investigating biology. The C. elegans Sequencing Consortium."; Science 282:2012-2018(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
STRAIN=Bristol N2;
Wormbase Consortium;
Submitted (SEP-2004) to the EMBL/GenBank/DDBJ databases.
Submitted (SEP-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; U42846; AAA83600.2; -..
PIR; T16892; T16892.
RESP; P07996; L16892.
Resp; P07996; L16892.
Resp; P07996; L16892.
Resp; P1792.1; CE30185.
Resp; P0704212; Premetalloendopeptidase activity; IEA.
GO; GO:0006208; P: protecolysis and peptidolysis; IEA.
Repres; IPR006199; P: protecolysis and peptidolysis; IEA.
RinterPro; IPR00199; Psptidase M12B.
RinterPro; IPR000884; TSP1.
Repfan; PF00190; TRSP1.
Repfan; PF00190; TSP1.
Repfan; PF00190; TSP1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "The sequence of C. elegans cosmid T19D2.";
Submitted (JAN-1996) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Waterston R.; Submitted (NOV-2002) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                       632 AA; 69037 MW; 78CD7F28C3FFF3E7 CRC64;
                                                                                                                                                                                                                                                   Score 40; DB 2;
Pred. No. 13;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SMART; SM00209; TSP1; 4.
PROSITE; PS50215; ADAM_MEPRO; 1.
PROSITE; PS50092; TSP1; 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=Bristol N2;
MEDLINE=99069613; PubMed=9851916;
InterPro; IPR002165; Plexin_repeat.
                         InterPro; IPR000884; TSP1.
InterPro; IPR008085; TSP-1.
Pfam; PF01437; PSL1; 1.
Pfam; PR01705; TSP-1; 5.
PRINTS; PR01705; TSP1REPEAT.
SMART; SM00423; PSL1; 1.
SMART; SM00209; TSP1; 5.
                                                                                                                                                                                                                                                            67.8%;
                                                                                                                                                                                                                                                                                                                                                                                              151 WSSWAQCSTSCG 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
                                                                                                                                                                                                                                                                                      Local Similarity 50.0 les 6; Conservative
                                                                                                                                                                                                                                                                                                                                                6 WSXXXXXXXX 17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q22580
Q22580;
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RA Adachi J., Alzawa T., Arakawa T., Bono H., Carninci P., Adachi J., Alzawa K., Akimura T., Arakawa T., Hono H., Carninci P., Adachi J., Alzawa K., Akimura T., Haraka T., Hirozane T., Hirozane T., Hirozane T., Hayashida K., Hayatsu N., Hiramoto K., Hiracka T., Hirozane T., RA Hayashida K., Ishin Y., Icoh M., Kagawa I., Kaukawa T., RA Hori F., Imocani K., Ishin Y., Icoh M., Kagawa I., Kauka T., Ratoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S., RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M., Rakati R., Sakazume N., Sano H., RA Sasti C., Sakai K., Sakazume N., Sano H., Rayawa J., Shinagawa A., Shiraki T., Sogabe Y., Tagami M., Angawa A., Taya T., Yasumishi A., Muramatsu M., Hayashizaki Y.; A Tomaru A., Toya T., Yasumishi A., Muramatsu M., Hayashizaki Y.; RHSSP, P07996; ILSL.
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Saga Y., Nagase T., Ohara O., Koga H.;
Saga Y., Nagase T., Ohara O., Koga H.;
In the complete nucleotide sequences of 600 mouse KIAA-homologous
III. the complete nucleotide sequences of 500 mouse KIAA-homologous
III. the complete nucleotide sequences of cDNA clones
cDNAs identified by screening of terminal sequences of cDNA clones
randomly sampled from size-fractionated libraries.";
DNA Res. 10:167-180(2003).
RMBI, AKI29362; BAC98172.1; -
GO; GO.0005515; C:extracellular space; TAS.
GO; GO:0016021; C:integral to membrane; TAS.
InterPro; IPR003659; Plexin-like.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mus musculus (Mouse).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Mus
           Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A., Azamanco R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K., Fujiwake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M., Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J. Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.; HarkEN integrated sequence analysis (RISA) system-384-format sequencing pippeline with 384 multicapillary sequencer.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 40; DB 2; Length 478;
Pred. No. 11;
0; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE 478 AA; 51394 MW; F4A9DFF173F0A376 CRC64;
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InterPro; IPR000884; TSP1.
InterPro; IPR008085; TSP-1.
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Similarity 50.0%; Pred. No. 1
6; Conservative 0; Mismatch
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; PR01705; TSP1REPEAT.
SM00209; TSP1; 5.
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TISSUE=Embryonic tail;
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Best Local Similarity
Matches 6; Conserv
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Matches
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                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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                                    Score 40; DB 2; Length 872;
Pred. No. 18;
0; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HSSP; P07996; ILSL.
MGD; MGI:107556; Sema5a.
GG):GO:0016021; Ciintegral to membrane; IDA.
GG):GO:0008046; F:axon guidance receptor activity; IDA.
GG):GO:000741; P:axon guidance; IMP.
Interpro; IPR003659; Plexin-like.
Interpro; IPR00165; Plexin_repeat.
Interpro; IPR001627; Sema.
Interpro; IPR008044; TSP1.
Interpro; IPR008084; TSP1.
Ffam; PP01431; PSI; 1.
PROSITE; PS00142; ZINC_PROTEASE; UNKNOWN_1.
Hypothetical protein.
SEQUENCE 872 AA; 98040 MW; 1BAID480AEF0ED15 CRC64;
                                                                                                                                                     30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
35-OCT-2004 (Rel. 45, Last annotation update)
Semaphorin 5A precursor (Semaphorin F) (Sema F)
Name-Sema5a; Synonyms-Semaf, SemF;
Mus musculus (Mouse).
                                                                                                                                       PRT; 1077 AA.
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Pfam; PP001403; Sema; 1.
Pfam; PR01090; TSP 1; 5.
SMART; SM00422; PS1; 1.
SMART; SM0050; Sema; 1.
SMART; SM00209; TSP1; 6.
PROSITE; PS51004; SEMA; 1.
PROSITE; PS50092; TSP1; 6.
                                     67.8%;
50.0%;
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                           Ouery Match
Best Local Similarity 50.0
East Local Similarity 50.0
                                                                                          831 WSSWSSCSTKCG 842
                                                                        6 WSXXXXCSXXCG 17
                                                                                                                                      STANDARD;
                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
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Q62217;
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Straubberg R.L., Feingold B.A., Groues J.H., Dorge J.G.,
Riaunner R.D., Collins F.S., Wagner L.H., Dorge J.G.,
Altschul S.F., Zeeberg B. Buerow K.H., Schaefer C.F., Bhard N.K.,
Altschul S.F., Zeeberg B. Buerow K.H., Schaefer C.F., Bhard N.K.,
Hopkins R.F., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
A stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Brownstein M.J., Usdin T.B., Teenivuki S., Carninci P., Prange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Villalon D.K., Muzny D.W., Sodergen B.J., Lu X., Gibbs R.A.,
Whiting M., Madan A., Young A.C., Shevchenko Y., Boutfard G.G.,
Mitting M., Touchman J.W., Green B.D., Dickson M.C.,
A Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
Developmental protein; Glycoprotein; Multigene family; Neurogenesis;
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Xenopus laevis (African clawed frog).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
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MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 1; Length 1077;
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                                                                        Semaphorin 5A.
Extracellular (Potential)
                                                                                                                                          Cytoplasmic (Potential).
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TSP type-1 2.
TSP type-1 3.
TSP type-1 4.
TSP type-1 5.
TSP type-1 6.
TSP type-1 7.
By similarity.
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0; Mismatches
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N-linked
N-linked
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1077 AA;
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                         Repeat; Signal;
SIGNAL 1
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effort to identify novel human secreted and transmembrane proteins:
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SMSB_HUMAN
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SEQUENCE FROM N.A.
SEQUENCE TROM N.A.
SEQUENCE TROM N.A.
Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D., Brush J.,
Clark H.F., Gurney A.L., Crowley C., Currell B., Deuel B., Dowd P.,
Chow B., Choui C., Crowley C., Currell B., Deuel B., Dowd P.,
Eaton D., Foster J., Grimadid C., Gu Q., Hass P.E., Heldens S.,
Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J.,
Liao D., Mark M., Robbie E., Sanchez C., Schoenfeld J.,
Seshagiri S., Simmons L., Singh J., Smith V., Stinson J., Vagts A.,
Vandlen R., Watanabe C., Wieand D., Woods K., Xie M.H., Yansura D.,
Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A., Wood W.I.,
Goddwski P.;
                Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E., Jones S.J., Marra M.A.; "Generation and initial analysis of more than 15,000 full-length human
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Homo aspiens (Human).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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                                                                                                                                                                                            MEDLINE-22341132; PubMed=12454917; DOI=10.1002/dvdy.10174; Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W., Richardson P.; Richardson P.; "Genetic and genomic tools for Xenopus research: The NIH Xenopus
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Pred. No. 21;
0; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                 TISSUE=Embryo;
Klein S., Strausberg R.;
Submitted (OCT-2003) to the EMBL/GenBank/DDBJ databases.
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A; 122657 MW; 4DFCD371A7CD8176 CRC64;
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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
                                                                                         and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
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GO; GO: 0016020; C: membrane; IEA.
GO; GO: 00016272; F: receptor activity; IEA.
GO; GO: 0007275; P: development; IEA.
InterPro; IPR003659; Plexin_like.
InterPro; IPR0031627; Sema.
InterPro; IPR001627; Sema.
InterPro; IPR00884; TSP1.
Pfam; PF01407; PS1; 1.
Pfam; PF01407; PS1; 1.
Pfam; PF01403; Sema; 1.
Pfam; PR01403; Sema; 1.
SMART; SM00423; PS1; 1.
SMART; SM00439; TSP1; 6.
PROSITE; PS20092; TSP1; 6.
SMART; SM0050; TSP1; 6.
SMART; SM0050; TSP1; 6.
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50.0%;
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Best Local Similarity 50...
6; Conservative
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bloinformatics and the EMBL outstation the Buropean Bloinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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MRDLINE=20277482; PubMed=10819331;
Nagase T., Kikuno R., Ishikawa K.-I., Hirosawa M., Ohara O.;
Nagase T., Kikuno R., Ishikawa K.-I., Hirosawa M., Ohara O.;
Prediction of the coding sequences of unidentified human genes. XVII.
The complete sequences of 100 new cDNA clones from brain which code for large proteins in vitro.";
DNA Res. 7:143-150(2000).
-I- FUNCTION: May act as positive axonal guidance cues (By
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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Pred. No. 21;
0; Mismatches 6; Indels
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119322 MW; 082BF746687C0AC5 CRC64;
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--- SUBCELLULAR LOCATION: Type I membrane protein.
--- SIMILARITY: Belongs to the semaphorin family.
--- SIMILARITY: Contains 1 Sema domain.
--- SIMILARITY: Contains 7 TSP type-1 domains.
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10-OCT-2003 (Rel. 42, Last sequence update)
25-OCT-2004 (Rel. 45, Last annotation update)
Dioinformatics assessment.";
Genome Res. 13:265-2270 (2003).
Genome Res. 13:265-2270 (2003).
Genome Res. 13:265-2270 (2003).
GO; GO:0016020; C:membrane; IEA.
GO; GO:00016872; F:receptor activity; IEA.
GO; GO:0007275; P:development; IEA.
InterPro; IPR0020569; Plexin.like.
InterPro; IPR0020569; Plexin.repeat.
InterPro; IPR002069; FSP1.
InterPro; IPR008084; TSP1.
InterPro; IPR008085; TSP1.
INTERPRO; IPR0080865; TSP1.
INTERPRO; IPR0080865; TSP1.
INTERPRO* IPR0080865; TSP1.
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Genew; HGNC:10737; SEMA5B.
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Interpro; IPR002165; Plexin_repeat.
Interpro; IPR001627; Sema.
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Name=SEMA5B; Synonyms=KIAA1445;
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Best Local Similarity 50..
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CARBOHYD
SEQUENCE
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Q7QC32
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                                               Pfam; PF01403; Sema; 1.
Pfam; PF001403; Sema; 1.
Pfam; PF00090; TSP 1; 5.
PRINTS; PR01705; TSP 1; 5.
SWART; SW00423; PST; 1.
SWART; SW00209; TSP1; 5.
PROSITE; PS51004; SEMA; 1.
PROSITE; PS50092; TSP1; 5.
Developmental protein; Glycoprotein; Multigene family; Neurogenesis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDILINE-96414430; PubMed=8817451; DOI=10.1016/0925-4773(96)00525-4; Adams R.H., Betz H., Pueschel A.W.; An novel class of murine semaphorins with homology to thrombospondin is differentially expressed during early embryogenesis."; Mech. Dev. 57:33-451(199).
-!- FUNCTION: May act as positive axonal guidance cues.
-!- SUBCELLULAR LOCATION: Type I membrane protein.
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25-OCT-2004 (Rel. 45, Last annotation update)
25-OCT-2004 (Rel. 45, Last annotation update)
Semaphorin 5B precursor (Semaphorin G) (Sema G).
Name=Semabb; Synonyms=SEMAG, SemG;
Mus musculus (Mouse).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus.
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Pred. No. 21;
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Extracellular (Potential)
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50.0%;
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                InterPro; IPR008085; TSP_1.
Pfam; PF01437; PSI; 1.
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Best Local Similarity
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Q60519;
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TRANSMEM .
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the BMBL outstation the Buropean Bioinformatics Institute. The Buropean Bioinformatics Institute. The Buropean Bioinformatics Institute. The Buropean Bioinformatics Institute are no restrictions on its by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb.sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                     MGD; MGI:107555; Sema5b.

R InterPro; IPR003659; Plexin-like.

R InterPro; IPR001627; Sema.

R InterPro; IPR001627; Sema.

R InterPro; IPR001627; Sema.

R InterPro; IPR001627; Sema.

R InterPro; IPR001684; TSP1.

R InterPro; IPR008085; TSP1.

R Pfam; PF01437; PSI; 1.

R Pfam; PF00403; Sema; 1.

R Pfam; RMAT; SM00209; TSP1; 5.

R SMART; SM00209; TSP1; 5.

R SMART; SM00209; TSP1; 5.

R PROSITE; PS51004; SEMA; 1.

R PROSITE; PS51004; SEMA; 1.

R PROSITE; PS51004; GSPA; 1.

R PROSITE; PS51004; GSPA; 1.

R PROSITE; PS51004; GSPA; 1.
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-!- TISSUE SPECIFICITY: In adult, only detected in brain.
-!- DEVELOPMENTAL STAGE: Differentially expressed in embryonic and adult tissues. Its abundance decreases from E10 to birth.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (Potential) (Potential)
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Semaphorin 5B.
Extracellular (Potential)
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                                           adult tissues. Its abundance decreases from E-1- SIMILMARIY: Balongs to the semaphorin family.-!- SIMILMARIY: Contains 1 Sema domain.-!- SIMILMARIY: Contains 7 TSP type-1 domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    . 9
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Pred. No. 21;
0; Mismatches
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TSP type-1 2
TSP type-1 4
TSP type-1 5
TSP type-1 6
TSP type-1 6
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Best Local Similarity 50.0
Matches 6; Conservative
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DEDITION (Fragment).

Name-ebiG1179; ORFNames=ENSANGG000001015;

Anopheles gambiae str. PEST.

Bukaryota, Metazoa, Arthropoda; Hexapoda; Insecta; Pterygota;

Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Anopheles.

NCBI_TaxID=180454;
                                                                                                                                                                                                                              Anopheles Genome Sequencing Consortium,
Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
-!- CAUTION: The sequence shown here is derived from an
EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
preliminary data.
EMBL; AAAB01008859; EAA07529.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 67.8%; Score 40; DB 2; Length 1093; Best Local Similarity 50.0%; Pred. No. 21; Matches 6; Conservative 0; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1093 1093 AA; 118842 MW; 2DB86BEC7CB42230 CRC64;
Q7QC32 PRELIMINARY; PRT; 1093 AA. 207C32; Q1C92 (TrEMBLrel. 26, Created) 01-MAR-2004 (TrEMBLrel. 26, Last sequence update) 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
                                                                                                                                                                                                                                                                                                                                           GO; GO: 0016020; C: membrane; IEA.
GO; GO: 0004872; F: receptor activity; IEA.
InterPro; IPR002165; Plexin_repeat.
InterPro; IPR001627; Sema.
InterPro; IPR001884; TSP1.
InterPro; IPR008884; TSP1.
Pfam; PF01437; PSI; 1.
Pfam; PF01437; PSI; 1.
Pfam; PF01403; Sema; 1.
Pfam; PF01403; Sema; 1.
PRINTS; PR01705; TSP1; 5.
                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                 STRAIN-PEST;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NON TER
NON TER
SEQUENCE
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Search completed: April 1, 2005, 13:59:24 Job time: 139.696 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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OM protein - protein search, using sw model

Run on:

April 1, 2005, 13:43:07; Search time 30.6087 Seconds (without alignments) 69.156 Million cell updates/sec

1 XXXXXWSXXXXCSXXCGXXXXX 22 US-09-462-909D-9 59 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283416 seqs, 96216763 residues Searched:

283416 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

1: pirl:* 2: pir2:* 3: pir3:* 4: pir4:* .Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description		nypornerical proce		thrombospondin 1 p	coccidiosis-relate	hypothetical prote		c	antigen Em100 - Ei	hypothetical prote		brain-specific and	protein CTRP - mal	hypothetical prote	pre	F-spondin - rat	hypothetical prote		•+	thrombospondin 2 p	thrombospondin pre	cartilage intermed	procollagen N-endo	brain-specific and	properdin - mouse	hypothetical prote		hypothetical prote		hypothetical prote
SUMMARIES	Tì 6000	260011	ISHUPI	A40558	A45517	T16761	T29247	A45638	A48569	T00326	T18856	T00028	T18397	T25061	A47723	A38152	T15976	JC5928	TSHUP2	A42587	A39804	T09484	T18517	T00026	S05478	T16557	T34212	T33922	T00027	T22545
Length DB								712 2											1172 1								805 2	0	a	1059 2
\$ Query Match I	67.0		0.10	1	66.1	66.1	66.1	66.1	66.1	66.1	66.1	66.1	66.1	64.4	64.4	64.4	64.4	64.4	64.4	64.4	64.4	64.4	64.4	64.4	N	62.7	62.7	62.7	62.7	59.3
Score			2	40	39	39	39	39	39	39	39	39	39	38	38	38	38	38	38	38	38	38	38	38	37	37	37	37	37	35
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plectoxin X - spid TRAP-C2 protein - brootherical prote	hypothetical prote hypothetical prote unc-5 protein - Ca	unc-5 protein, lon hypothetical prote thrombospondin-rel	sporozoite surface hypothetical prote hypothetical prote	hypothetical prote properdin precurso hypothetical prote	
H53613 S49108 T20523	T20524 T19477 T32541	B44294 T28846 S04531	A46283 T04191 T19366	T21371 S29126 T47158	T00355
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49 123 293	334 651 919	947 291 559	574 703 736	2165 469 550	837
57.6	57.6 57.6 57.6	57.6 55.9	55.9	54.2	54.2
60 60 60 44 44 44	. W W W	6. 6. 6. 4. 6. 6.		9 2 3	35
3 3 3 3 3 3 3		36 38	39 4 4 0 1 1	4 4 4 0 6 4	45

ALIGNMENTS

RESULT 1 T1692 T1692 hypothetical protein T19D2.1 - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004 C;Accession: T16892 R;Bentley, D. Submitted to the EMBL Data Library, December 1995 A;Description: The sequence of C. elegans cosmid T19D2.
 A;Status: preliminary; translated from GB/EMBL/DDBJ A;Molecule type: DNA A;Residues: 1-860 <ben> A;Cross-references: UNIPROT:Q22580; EMBL:U42846; NID:g1125809; PID:g1125810; PIDN:AAA8360</ben>
 Cjecucics: A;Gene: CESP:T19D2.1 A;Introns: 56/3; 96/1; 171/3; 199/3; 245/2; 293/2; 335/3; 395/3; 426/3; 484/2; 505/3; 587
 Query Match 67.8%; Score 40; DB 2; Length 860; Best Local Similarity 50.0%; Pred. No. 4.2; Matches 6; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

831 WSSWSSCSTKCG 842 6 WSXXXXCSXXCG 17 ઠે 셤

Cispecies: Home sapiens (man)
Cispecies: J3-Aug-1997 #sequence_revision 03-Aug-1995 #text_change 09-Jul-2004
Cidension: A26155; A34274; A30140; A25812; A65172; A42927
Ricawler, J.; Hymes, R.O.
J. Call Biol. 103, 1635-1648, 1986
A;ritle: The structure of human thrombospondin, an adhesive glycoprotein with multiple cs A;reference number: A26155; MUID:87057617; PMID:2430973
A;Accession: A26155
A;Accession: A26155
A;Accession: A26155
A;Accession: Dispective (man)
A;Residues: 1-1170 < LAW>A;Residues: 1-1170 < LAW>A;Residues: 1-1170 < LAW>A;Accession: Dispective (man)
A;Cross-references: UNIPROT:P07996; GB:X04665; NID:g37137; PIDN:CAA28370.1; PID:g37138
A;Accessore (man)
A;Accessor

A;Accession: A34274 A;Molecule type: DNA A;Rolecule type: LNA A;Cross-references: GB:J04835 R;Hennessy, S.W.; Frazier, B.A.; Kim, D.D.; Deckwerth, T.L.; Baumgartel, D.M.; Rotwein, F

```
R;Lawler, J.; Duquette, M.; Ferro, P.; Copeland, N.G.; Gilbert, D.J.; Jenkins, N.A. Genomics 11, 587-600, 1991
A;Title: Characterization of the murine thrombospondin gene.
A;Reference number: A40558
A;Reference number: A40558
A;Status: preliminary
A;Molecule type: DRA
A;Residues: 1-1170 <LAM>A;Residues: 1-1170 <LAM>A;Residues: 1-1170 <LAM>A;Residues: 1-1170 <LAM>A;Residues: 1-1170 <LAM
A;Residues: 1-1170 -LAM
A;Residues: UNIPROT:P35441; GB:MG2469; GB:MG2451; GB:MG2452; GB:MG2452; GB:MG2464; GB:MG2464; GB:MG2465; GB:MG2466; GB:MG2468; GB:MG2469; GB:MG2469;
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C,Complex: homotrimer, disulfide linked
C,Complex: homotrimer, disulfide linked
C,Superfamily: thrombospondin 1; EGF homotrimer
C,Reywords: calcium binding; glycoprotein; homotrimer
F,1-18/Domain: signal sequence #status predicted <SIG>
F,19-1170/Product: thrombospondin 1 #status predicted <AMT>
F,31-375/Domain: thrombospondin type 1 repeat homology <THR1>
F,318-429/Domain: thrombospondin type 1 repeat homology <THR2>
F,314-490/Domain: thrombospondin type 1 repeat homology <THR2>
F,51-586/Domain: EGF homology <EGF>
F,51-586/Domain: EGF homology <EGF>
F,51-586/Domain: EGF homology <EGF>
F,51-586/Domain: EGF homology <EGF>
F,51-586/Domain: Accordance (Asn) (covalent) #status predicted
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A, Fetture: Preliminary, not compared with conceptual translation
A, Molecule type: mRNA
A, Residues: 1-1152, P'. 1154-1170 < LAH>
A, Fessidues: 1-1152, P'. 1154-1170 < LAH>
A, Forsa-references: GB: MB37276
A, Mote: sequence extracted from NCBI backbone (NCBIP:81501)
R, Mote: sequence extracted from NCBI backbone (NCBIP:81501)
R, Mote: sequence extracted from NCBI backbone (NCBIP:81501)
A, Mote: sequence extracted from NCBI backbone (NCBIP:81501)
A, Title: Expression and initial characterization of recombinant mouse thrombospondin 1 ar
A, Reference number: S68787; MUID:96234006; PMID:8654563
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NyAlternate names: thrombospondin-related antigen, 100K
NyAlternate names: thrombospondin-related antigen, 100K
C;Species: Eimeria tenella
C;Species: O3-Unn-1993 #sequence_revision O3-Unn-1993 #text_change O9-Jul-2004
C;Accession: A45517; S27818
R;Clarke, L.E.; Tomley, F.M.; Wisher, M.H.; Foulds, I.J.; Boursnell, M.E.G.
Mol. Biochem: Parasitol. 41, 269-280, 1990
A;Aitle: Regions of an Eimeria tenella antigen contain sequences which are conserved in A;Reference number: A45517; MUID:90377296; PMID:2204833
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A.Cross-references: GB:J05605; GB:J05606; NID:g201991; PIDN:AAA40431.1; PID:g554390
R.Lahorty, C.D.; O'Rourke, K.; Wolf, F.W.; Katz, R.; Seldin, M.F.; Dixit, V.M.
J. Biol. Chem. 267, 3274-3281, 1992
A.Fitle: Characterization of mouse thrombospondin 2 sequence and expression during cell A.Reference number: A42587; MUID:92147683; PMID:1371115
A.Accession: B42587
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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Pred. No. 5.2;
0; Mismatches 6; Indels
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Best Local Similarity 50.0%;
Matches 6; Conservative
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Molecule type: DNA
Residues: 1-206 <CLA>
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A;Molecule type: DNA
A;Residues: 1-490 <BOR>
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A, Accession: A4227.

A, Molecule type: protein

A, Readdues: 997-1003 <SUN>
A, Note: Cys-992 is shown to have a free sulfhydryl

C, Genetics: A, Gene: GDB:120438; OMIM:188060

A, Introns: 23/1

A, Introns: 23/1

A, Note: the list of introns may be incomplete
C; Complex: homotrimer, disulfide linked
C; Function:
A, Description: participates in cell migration and adhesion, and in platelet aggregation
A, Description: participates in cell migration and adhesion, and in platelet aggregation
C; Superfamily: thrombospondin 1; EGF homology; thrombospondin type 1 repeat homology; vC
C; Keywords: beta-hydroxyasparagine; calcinum binding; cell adhesion; glycoprotein; trimer
C; Keywords: beta-hydroxyasparagine; calcinum binding; cell adhesion; glycoprotein; trimer
C; Keywords: beta-hydroxyasparagine; calcinum binding; cell adhesion; glycoprotein; trimer
F; 19-1170/Product: thrombospondin 1 #status predicted <MAT>
F; 19-1170/Product: thrombospondin type 1 repeat homology <THR2>
F; 375-1586/Domain: thrombospondin type 1 repeat homology <THR2>
F; 434-490/Domain: EGF homology <EGF2>
F; 515-1586/Domain: EGF homology <EGF2>
F; 525-1586/Domain: EGF homology <EGF2>
F; 526-528/Region: cell attachment (R-G-D) motif
F; 71-232/Disulfide bonds: interchain #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Molecule type: mRNA A; Molecule type: machine the mature of this sequence, including the amino end of the mature protein, were determined to this sequence, molecule D. F. A; Molecule type: Molecule type: Molecule type: Molecule type: MID: Molecule type: MID: Molecule type: MID: Molecule type: MID: MID: Molecule type: MID: MID: MID: MID: MID: 1379247
                                                                   J. Cell Biol. 108, 729-736, 1989
A;Title: Complete thrombospondin mRNA sequence includes potential regulatory sites in th A;Reference number: A30140; MUID:89139590; PMID:2918029
A;Accession: A30140
A;Accession: A30140
A;Accession: BRNA
A;Residues: 1-83,'A','85-522,'A',524-1170 CHEN>
A;Residues: 1-83,'A','85-522,'A',524-1170 CHEN>
A;Residues: Legala,'A','85-522,'A', FUID:937464; PIDN:CAA12889.1; PID:937465
A;Rote: parts of this sequence, including the amino end of the mature protein, were dete R;Kobayashi, S.; Eden-McCutchan, F.; Framson, P.; Bornstein, P.
Biochemistry 25, 8418-8425, 1986
A;Title: Partial amino acid sequence of human thrombospondin as determined by analysis of A;Reference number: A25812; MUID:87157592; PMID:3030396
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C;Species: Mus musculus (house mouse)
C;Date: 05-Jun-1992 #sequence_revision 05-Jun-1992 #text_change 09-Jul-2004
C;Accession: A40558; A37905; B42587; S68787
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A; Residues: 1-83, A', 85-397 < KOB>
A; Cross-references: GB: M25631; NID: 9538353; PIDN: AAA36741.1; PID: 9538354
R; Dixit, V. W.; Hennessy, S.W.; Grant, G.A.; Rotwein, P.; Frazier, W.A.
Proc. Natl. Acad. Sci. U.S.A. 83, 549-5453, 1986
A; Reference number: A05172; MUID: 86287276; PMID: 3461443
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Pred. No. 5.2;
0; Mismatches 6; Indels
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Best Local Similarity 50.0%;
Matches 6; Conservative
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R;Tomley, F.M.; Clarke, L.E.; Kawazoe, U.; Dijkema, R.; Kok, J.J.
Mol. Biochem. Parasitol. 49, 277-288, 1991
A;Title: Sequence of the gene encoding an immunodominant microneme protein of Eimeria ter
A;Reference number: A45638; MUID:92131064; PMID:1775171
                                                                                                                                                                                                                                                                                                                                        A; Molecule type: DNA
A; Mesidues: 1-712 CTOM>
A; Mesidues: 1-712 CTOM>
A; Cross-references: UNIPROT:043981; GB:AF032905; GB:M73485; NID:g2707732; PIDN:AAD03350.1
A; Oross-references: UNIPROT:043981; GB:AF032905; GB:M73485; NID:g2707732; PIDN:AAD03350.1
A; Note: sequence extracted from NCBI backbone (NCBIN:77752, NCBIP:77756)
F; A9 = 218 Domain: thrombospondin type 1 repeat homology CTHR2>
F; A9 = 236 / Domain: thrombospondin type 1 repeat homology CTHR3>
F; A7 = 432 / Domain: thrombospondin type 1 repeat homology CTHR3>
F; A94 = 556 / Domain: thrombospondin type 1 repeat homology CTHR6>
F; 560-610 / Domain: thrombospondin type 1 repeat homology CTHR6>
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R;Pasamontes, L.; Hug, D.; Humbelin, M.; Weber, G.
Mol. Biochem. Parasitol. 57, 171-174, 1993
MyIttle: Sequence of a major Eimeria maxima antigen homologous to the Eimeria tenella mic A;Title: Sequence of a Mujor Eimeria maxima antigen homologous to the Eimeria tenella mic A;Title: A48569; MuID:93149203; PMID:8426611
A;Racession: A48569
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A;Title: Prediction of the coding sequences of unidentified human genes. IX. The complete A;Reference number: 214086; MUID:98290545; PMID:9628581
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C;Date: 01-Feb-1999 #sequence_revision 01-Feb-1999 #text_change 15-Mar-2004
    22-Apr-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
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A;Note: sequence extracted from NCBI backbone (NCBIN:123776, NCBIP:123777)
F;45-218/Domain: von Willebrand factor type A repeat homology «VWA2>
F;238-296/Domain: thrombospondin type I repeat homology «THRI>
F;309-371/Domain: thrombospondin type I repeat homology «THRI>
F;372-432/Domain: thrombospondin type I repeat homology «THRI>
F;431-493/Domain: thrombospondin type I repeat homology «THRA>
F;443-4956/Domain: thrombospondin type I repeat homology «THRA>
F;560-610/Domain: thrombospondin type I repeat homology «THRA>
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Pred. No. 5.7;
0; Mismatches 6; Indels
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Pred. No. 5.6;
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50.0%;
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A;Molecule type: nucleic acid
A;Residues: 1-724 <PAS>
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Best Local Similarity
Matches 6; Conserv
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Matches 6; Conserv
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A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Status: preliminary;
A;Residues: 1-610 <FUL>
A;Cross-references: EMBL:U00036; NID:g458996; PID:g459001; PIDN:AAA50653.1; CESP:R151.5
A;Experimental source: strain Bristol N2
C;Genetics:
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A;Introne: 89/3; 138/3; 192/3; 260/1; 312/1; 400/2; 445/3; 496/1; 523/1; 558/2; 596/2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            hypothetical protein R151.5 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Dec-2002
C;Accession: T16761
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Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
                                                                                                                                                                               Gaps
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A;Introns: 68/3; 120/1; 151/1; 307/1; 448/2; 525/2; 567/2; 592/2
C;Superfamily: metalloproteinase hch-1; astacin homology
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F;136-198/Domain: thrombospondin type 1 repeat homology <THR5>
                                                                                                                                                                               Indels
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R;Minx, P.; Hawkins, J.
R;Minx, P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Rifulton, L. submitted to the EMBL Data Library, February 1994 submitted to the EMBL Data Library, February 1994 Albecription: The sequence of C. elegans cosmid R151. AlReference number: 844639
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C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence revision 15-Oct-1999 #+*
                                                                                     Score 39; DB 2;
Pred. No. 2.4;
0; Mismatches
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A;Molecule type: DNA
                                                                                          66.1%;
50.0%;
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                                                                                     Query Match
Best Local Similarity 50.0
Matches 6; Conservative
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A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Status: DNA
A;Molecule type: DNA
A;Residues: 1-2098 <TRO>
A;Cross-references: UNIPROT:Q25757; EMBL:U34363; NID:g1098897; PID:g1098898; PIDN:AAC4696.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    protein CTRP - malaria parasite (Plasmodium falciparum)
C;Species: Plasmodium falciparum
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T18397
R;Trottein, F.; Triglia, T.; Cowman, A.F.
Mol. Biochem. Parasitol: 74, 129-142, 1995
A;Trile: Molecular cloning of a gene from Plasmodium falciparum that codes for a protein A;Reference number: Z18926; MUID:96366471; PMID:8719155
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A;Molecule type: DNA
A;Reaidues: 1-788 <WIL>
A;Residues: 1-788 <WIL>
A;Cross-references: UNIPROT: Q22631; EMBL: Z68011; PIDN: CAA92014.1; GSPDB: GN00028; CESP: T2
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C.Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C.Accession: T25061
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Pred. No. 9.5;
0; Mismatches 6; Indels
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                               A,Gene: GDB:BAI3
A,Crose-references: GDB:9838090; OMIM:602684
A,Map position: 6q12-6q12
F,344-398/Domain: thrombospondin type 1 repeat homology <THR3>
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submitted to the EMBL Data Library, November 1995
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A; Introns: 20/1; 47/1; 76/1; 152/1; 735/2; 754/2
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C;Species: Xenopus laevis (African clawed frog)
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Best Local Similarity 50.0%;
Matches 6; Conservative
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Best Local Similarity 50.0%;
Matches 6; Conservative
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A; Accession: T25061
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A,Gene: CESP:T21B6.3
C;Genetics:
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NyAlternate names: BAI3 protein
NyAlternate names: BAI3 protein
C;Species: Homo sapiens (man)
C;Date: 22-Jan-1999 #sequence_revision 22-Jan-1999 #text_change 09-Jul-2004
N;Shiratsuchi; T; Nishimori, H; Ichise, H; Nakamura, Y; Tokino, T.
Cytogenet. Cell Genet. 79, 103-108, 1997
A;Title: Cloning and characterization of BAI2 and BAI3, novel genes homologous to brain-A;Title: Cloning and characterization of BAI2 and BAI3, Accession: T00028
A;Accession: T00028
A;Accession: T00028
A;Accession: T00028
A;Accession: T00028
A;Residues: 1-1522 c8H1>
A;Coss-references: UNIPROT:O60242; EMBL:AB005299; NID:g3021700; PIDN:BAA25363.1; PID:g3
A;Experimental source: brain
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A;Map position: X
A;Introns: 25/3; 70/3; 96/3; 139/3; 187/1; 234/2; 282/3; 376/2; 422/2; 478/3; 509/3; 566
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                       A,Cross-references: EMBL:AB011122; NID:g3043623; PIDN:BAA25476.1; PID:g3043624 A;Experimental source: brain C;Genetics:
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A;Cross-references: EMBL:Z50006; PIDN:CAA90302.1; GSPDB:GN00028; CESP:C02B4.1
A;Experimental source: clone T07C5
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Pred. No. 9.1;
0; Mismatches 6; Indels
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A;Note: KIAA0550
F;344-398/Domain: thrombospondin type 1 repeat homology <THR3>
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A,Molecule type: DNA
A;Status: preliminary; translated from GB/EMBL/DDBJ
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50.0%;
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Best Local Similarity 50.0%;
Matches 6; Conservative
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nes 6; Conserva
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C; Accession: A47723
R; Ruiz i Altaba, A.; Cox, C.; Jessell, T.M.; Klar, A.
Proc. Natl. Acad. Sci. U.S.A. 90, 8268-8272, 1993
A; Title: Ectopic neural expression of a floor plate marker in frog embryos injected with A; Reference number: A47723; MUID: 93376785; PMID: 8367492
A; Accession: A47723
A; Accession: A47723
A; Accession: A47723
A; Residues: 1-803 < RUI>
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C;Species: Rattus norvegicus (Norway rat)
C;Accession: A38152
C;Accession: A.; Baldassare, M.; Jessell, T.M.
R;Klar, A.; Baldassare, M.; Jessell, T.M.
Cell 69, 95-110, 1992
A;Title: F-spondin: a gene expressed at high levels in the floor plate encodes a secrete A;Accession: A38152; MUD:92208952; PMID:1555244
A;Accession: A38152
A;Status: preliminary
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Residues: 1-807 < KLA>
A;Cross-references: UNIPROT:P35446; GB:M88469; NID:g204176; PIDN:AAA41174.1; PID:g204177
A;Experimental source: embryo floor plate
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C;Date: 27-Jun-1994 #sequence_revision 27-Jun-1994 #text_change 09-Jul-2004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Note: sequence extracted from NCBI backbone (NCBIN:90877, NCBIP:90878) (Superfamily: F-spondin; thrombospondin type I repeat homology THR2> F;41-495/Domain: thrombospondin type I repeat homology THR3> F;500-555/Domain: thrombospondin type I repeat homology THR3> F;557-611/Domain: thrombospondin type I repeat homology THR4> F;57-611/Domain: thrombospondin type I repeat homology THR1> F;67-721/Domain: thrombospondin type I repeat homology THR1> F;67-721/Domain: thrombospondin type I repeat homology THR5> F;753-807/Domain: thrombospondin type I repeat homology THR5>
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64.4%; Score 38; DB 2; Length 803;
Best Local Similarity 50.0%; Pred. No. 9.4;
Matches 6; Conservative 0; Mismatches 6; Indels
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Pred. No. 9.4;
0; Mismatches 6; Indels
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50.0%;
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Best Local Similarity
Matches 6; Conserv
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A38152
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Search completed: April 1, 2005, 14:00:31 Job time : 31.6087 secs

620 WSEWSDCSVTCG 631

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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OM protein - protein search, using sw model
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April 1, 2005, 13:59:39 ; Search time 113.348 Seconds (without alignments) 64.360 Million cell updates/sec Run on:

US-09-462-909D-9 59

1 XXXXXWSXXXXCSXXCGXXXXX 22 Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

1413372 Total number of hits satisfying chosen parameters: 1413372 segs, 331592847 residues Searched:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

/cgn2_6/prodata/2/pubpaa/US06_NEW PUB.pep:*
/cgn2_6/prodata/2/pubpaa/US06_PUBGOMB.pep:*
/cgn2_6/prodata/2/pubpaa/US07_NEW PUB.pep:*
/cgn2_6/prodata/2/pubpaa/US08_NEW PUB.pep:*
/cgn2_6/prodata/2/pubpaa/US08_NEW PUB.pep:*
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/cgn2_6/prodata/2/pubpaa/US08_NEW PUB.pep:*
/cgn2_6/prodata/2/pubpaa/US08_PUBGOMB.pep:* /ptodata/2/pubpaa/US07_PUBCOMB.pep: 6/ptodata/2/pubpaa/PCT NEW PUB.pep /cgn2_6/1 /cgn2_6/1 /cgn2_6/1 /cgn2_6/1

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	Sequence 11, Appl	Sequence 6, Appli	9	Sequence 6, Appli	Sequence 35, Appl	Sequence 1454, Ap	Sequence 43, Appl	Sequence 20, Appl	-			111	114,
ΔΙ	US-10-042-696-11	US-09-373-658-6	9-189-686-60-SD	US-10-019-065A-6	US-10-883-144-35	US-10-276-774-1454	US-10-419-462-43	US-10-296-733-20	US-10-782-968-43	US-10-036-869-1	US-10-454-246-20	US-10-190-115-111	US-10-190-115-114
1	14	10	11	15	11	15	15	16	11	13	11	15	15
* Query Match Length DB	23	50	20	20	51	143	170	170	170	218	397	401	401
% Query Match	67.8	67.8	67.8	67.8	67.8	67.8	67.8	67.8	67.8	67.8	67.8	67.8	67.8
Score	40	40	40	40	40	40	40	40	40	40	40	40	40
Regult No.	-	7	m	4	S	9	7	æ	6	10	11	12	13

Sequence 116, App Sequence 118, App Sequence 10, Appl	Sequence 12, Appl Sequence 14, Appl	16,		Sequence 1047, Ap	Sequence 70, Appl	01 (Sequence 98, Appl	Sequence 16, Appl	Sequence 14, Appl	Sequence 14, Appl		Sequence 6, Appli	Sequence 2, Appli	'n	Sequence 43, Appl	Sequence 43, Appl	¥	æ	96	96	Sequence 96, Appl	96	96	96	Sequence 96, Appl
US-10-190-115-116 US-10-190-115-118 US-10-454-246-10	US-10-454-246-12 US-10-454-246-14	US-10-454-246-16 US-10-741-600-1020		₽			US-09-939-853A-98 TR-09-854-845-16		Þ	US-10-833-509-14	US-09-854-845-6	US-10-833-509-6	Þ	US-10-833-509-2			US-09-854-845-8	US-10-833-509-8			-	US-10-245-107-96	US-10-245-143-96	US-10-245-771-96	US-10-245-851-96
15	17	17	17	او	14	11:	٦,	17	σ	17	σ	17	σ	17	15	15	0	17	14	14	14	14	14	14	14
401 401 401	401	401 432	432	466	909	831	831 939	939	954	954	1034	1034	1049	1049	1077	1077	1078	1078	1092	1092	1092	1092	1092	1092	1092
67.8 67.8 67.8	67.8 67.8	67.8	67.8	67.8	67.8	67.8	67.9	67.8	67.8	67.8	67.8	67.8	67.8	67.8	67.8	67.8	67.8	67.8	67.8	67.8	67.8	67.8	67.8	67.8	67.8
4 4 4 0 0 0	4 4 0 0	4 4 0 0	0 4	4.0	40	0 4	4, 4 O C	40	40	40	40	40	40	40	40	40	40	40	40	40	40	40	40	40	40
14 15 16	17	19 20	21	23	24	25	270	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

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Sequence 11, Application US/10042696

Publication No. US20030171298A1

GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
TAPLICANT: Williams, Taffy
APPLICANT: Page
APPLICANT: Page
CURRENT FILING DATE: 2001-10-03
NUMBER OF SEQ ID NOS: 38
SOFTWARE: Patentin Ver 2.0
SEQ ID NO 11
LENGTH: 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: synthetic fragment/analog of
OTHER INFORMATION: thrombospondin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT ORGANISM: Artificial Sequence
RESULT 1
US-10-042-696-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-10-042-696-11
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RESULT 2 US-09-373-658-6 ; Sequence 6, Application US/09373658 ; Publication No. US20030092900A1 6 WSXXXXCSXXCG 17 4 WSEWTSCSTSCG 15 δ d

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Gaps

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67.8%; Score 40; DB 14; Length 23; 50.0%; Pred. No. 6.7; 6; Indels ative 0; Mismatches 6; Indels

6; Conservative

Query Match Best Local Similarity Matches 6, Conserva

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Query Match
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| Sequence 6, Application US/10019065A
| Sequence 6, Application US/10019065A
| Publication No. US20040086501A1
| GENERAL INFORMATION:
| APPLICANT: Bayer Corporation
| TITLE OF INVENTION: Protein Having Activity As An Angiogenesis Modulator
| TILE OF INVENTION: Protein Having Activity As An Angiogenesis Modulator
| PILE REFERENCE: MSB-7265-PCT |
| CURRENT APPLICATION NUMBER: US/10/019,065A |
| PRIOR APPLICATION NUMBER: US 60/266,330 |
| PRIOR PILING DATE: 2002-08-30 |
| NUMBER OF SEQ ID NOS: 34 |
| SOFTHARE: Patentin version 3.1 |
| SEQ ID NO 6 |
| LENGTH: 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
APPLICANT: Hatings, Gregg A.
APPLICANT: Ruben, Steven M.
APPLICANT: Ruben, Steven M.
APPLICANT: Jonak, Zdenka L.
APPLICANT: Torili, Stephen H.
APPLICANT: Trulli, Stephen H.
APPLICANT: Terrett, Jonathan A.
APPLICANT: Terrett, Jonathan A.
TILE OF INVENTION: Methl and Meth. Polynucleotides and Polypeptides
FILE REFERENCE: 1488.1070006
CURRENT FILING DATE: 1999-08-13
NUMBER OF SEQ ID NOS: 125
SEQ ID NOS: 125
SEQ ID NO 6
LENGTH: 50
TYPE: ...
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Hastings, Gregg A. APPLICANT: Ruben, Steven M. TITLE OF INVENTION: Methl and Meth2 Polynucleotides and Polypeptides TITLE OF INVENTION: Methl and Meth2 Polynucleotides and Polypeptides CHIES TERENCE: 1408-100000D CURRENT APPLICATION NUMBER: US/09/989,687 CURRENT FILING DATE: 2001-11-21 NUMBER OF SEQ ID NOS: 126 SOFTWARE: PATENTIN Ver. 2.0 SEQ ID NO 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 40; DB 11; Length 50;
Pred. No. 12;
0; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     67.8%; Score 40; DB 10; Length 50; 50.0%; Pred. No. 12; ive 0; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 6, Application US/09989687; Publication No. US20040002449A1; GENERAL INFORMATION:
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50.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           , ORGANISM: Homo sapiens
US-09-373-658-6
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hes 6; Conserva
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Best Local Similarity
Matches 6; Conserv
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Best Local S
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Sequence 35, Application US/10883144
; Sequence 35, Application US/20050634829A1
; Publication No. US20050054829A1
; GENERAL INFORMATION: CORPORATION
; APPLICANT: IMMUNEX CORPORATION
; APPLICANT: VAKII, Jalaleddin
; TITLE OF INVENTION: COMPOSITIONS AND METHODS RELATING TO TSP-30a, b, c AND d
; TILLE OF INVENTION: COMPOSITIONS AND METHODS RELATING TO TSP-30a, b, c AND d
; TILLE REFERENCE: 3474-A
; CURRENT FILLING DATE: 2004-07-01
; PRIOR PILLING DATE: 2004-07-01
; PRIOR PILLING DATE: 2003-07-22
; NUMBER OF SEQ ID NOS: 85
; SOFTWARE: PatentIn version 3.2
; LENGTH: 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 1454, Application US/10276774
; Sequence 1454, Application US/10276774
; Publication No. US20040053245A1
; GENERAL INFORMATION:
; APPLICANT: Hyeeq, Inc.
; APPLICANT: Tang, Y, Tom et al
; TITLE OF INVENTION: NO. US20040053245A1e1 Nucleic Acids and Polypeptides
; TITLE OF INVENTION: NO. US20040053245A1e1 Nucleic Acids and Polypeptides
; TIRE REFERENCE: 21272-030
; CURRENT APPLICATION NUMBER: US/10/276,774
; CURRENT FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: 09/496,914
PRIOR APPLICATION NUMBER: 09/496,914
PRIOR FILING DATE: 2000-02-03
; NUMBER OF SEQ ID NOS: 2700
; SOFTWARE: Custom
; SEQ ID NO 1454
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; TYPE: PRT; ORGANISM: Artificial Sequence; PRTURISM: PRTURE: PRTURE: OTHER INFORMATION: Isolated type 1 thrombospondin domain sequence: US-10-019-065A-6
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                                                                                                                               Score 40; DB 15; Length 50;
Pred. No. 12;
0; Mismatches 6; Indel8
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Pred. No. 12;
0; Mismatches 6
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Similarity 50.0%;
6; Conservative
                                                                                                                                      Query Match 67.8%;
Best Local Similarity 50.0%;
Matches 6; Conservative
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Best Local Similarity 50.0
Matches 6; Conservative
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT
CORGANISM: Homo sapien
US-10-883-144-35
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Matches 6; Conserv
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TITLE OF INVENTION: Thrombospondin Fragments and Uses Thereof In Clinical Assays for TITLE OF INVENTION: Thrombospondin Fragments and Uses Thereof In Clinical Assays for TITLE OF INVENTION: Cancer and Generation of Antibodies and Other Binding Agents FILE OF INVENTION: USOF OF 100 PRIOR PRIOR THING DATE: 2004-02-20 PRIOR APPLICATION NUMBER: US/10/419,462 PRIOR FILING DATE: 2003-04-21 NUMBER OF SEQ ID NOS: 53 SOFTWARE: Patentin version 3.2 LENGTH: 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 1, Application US/10036869
Publication No. US20020151516A1
GENERAL INFORMATION:
APPLICANT: Mixson, James A
TITLE OF INVENTION: CARRIER: DNA COMPLEXES CONTAINING DNA
TITLE OF THERAPY
THERAPY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                         OTHER INFORMATION: Thrombospondin Region plus Domain of type 1 repeats
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                              67.8%; Score 40; DB 17; Length 170; 50.0%; Pred. No. 29;
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Pred. No. 34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
SOFTWARE: Patentin Ralease #1.0, Version #1.25
CURRENT PATENTION DATA:
APPLICATION NUMBER: US/10/036,869
FILING DATE: 29-No. US20020151516A1-2001
CLASSIFICATION: «UNKNOWN»
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/985,526
FILING DATE: «UNKNOWN»
APPLICATION NUMBER: US 08/608,845
FILING DATE: 46-JUL-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES: 43
CORRESPONDENCE ADDRESS:
ADDRESSEE: Connolly, Bove, Lodge, & Hutz
STREET: 1220 Market Street, P.O. Box 2207
CITY: Wildington
STATE: Delaware
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE DESCRIPTION: SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: McMorrow Jr., Robert G
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ZIP: 19899
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ELEFAX: (302) 658-5613
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50.0%;
                                                                                                                                                                                                                                                                                   TYPE: PRT
ORGANISM: Artificial Sequence
       Williams, Kevin J.
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Best Local Similarity 50.07
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                  US-10-782-968-43
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US-10-036-869-1
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TITLE OF INVENTION: Thrombospondin Fragments and Uses Thereof In Clinical Assays for TITLE OF INVENTION: Cancer and Generation of Antibodies and Other Binding Agents FILE SEPERINCE: W1107-20005
CURRENT APPLICATION NUMBER: US/10/419,462
CURRENT APPLICATION NUMBER: US/10/419,462
SURRENT FILING DATE: 2003-04-17
NUMBER OF SEQ ID NOS: 53
SOFTWARE: Patentin version 3.2
SEQ ID NO 43
LENGTH: 170
TYPE: PAT
TYPE: PAT
ORGANISM: Artificial Sequence
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Pred. No. 29;
0; Mismatches 6; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 20, Application US/10296733
Publication No. US20040110131A1
GENERAL INFORMATION:
APPLICANT: Beth Israel Deaconess Medical Center
APPLICANT: Lawler, John W.
ITILE OF INVENTION: Thrombospondin-1 Type 1 Repeat
ITILE OF INVENTION: Thrombospondin-1 Type 1 Repeat
ITILE OF INVENTION: Polypeptides
CURRENT APPLICATION NUMBER: US/10/296,733
CURRENT FILING DATE: 2002-11-25
PRIOR FILING DATE: 2000-05-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQ ID NOS: 27
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 20
LENGTH: 170
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GENERAL INFORMATION: APPLICANT: Kevin J. Williams
                                                                                                                                                                Sequence 43, Application US/10419462 Publication No. US20040053392A1 GENERAL INFORMATION:
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50.0%;
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                                              89 WSSWALCSTSCG 100
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Best Local Similarity 50.0
Matches 6; Conservative
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6 WSXXXXXCSXXCG 17
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ORGANISM: Homo sapiens
US-10-296-733-20
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Best Local Similarity
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US-10-296-733-20
                                                                                                                  RESULT 7
US-10-419-462-43
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APPLICANT: Spadera, Steven K.
APPLICANT: Spadera, Steven K.
APPLICANT: Spadera, Steven K.
APPLICANT: Taupler, Raymond J. Jr.
APPLICANT: Taupler, Raymond J. Jr.
APPLICANT: Taupler, Raymond J. Jr.
APPLICANT: Zerbusen, Bryan D.
APPLICANT: Voss, Edward Z.
TITIB OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME FILE OF INVENTION NUMBER: 60/303,168
PRIOR APPLICATION NUMBER: 60/303,168
PRIOR APPLICATION NUMBER: 60/306,906
PRIOR APPLICATION NUMBER: 60/306,906
PRIOR APPLICATION NUMBER: 60/306,906
PRIOR PILING DATE: 2000-00-0
PRIOR PLING DATE: 2000-00-0
PRIOR PLING DATE: 2000-00-0
PRIOR PLING DATE: 2000-00-0
PRIOR PLING DATE: 2000-00-03
PRIOR APPLICATION NUMBER: 60/215,902
PRIOR PLING DATE: 2000-00-03
PRIOR PLING DATE: 2000-00-03
PRIOR PLING DATE: 2000-00-03
PRIOR PLING DATE: 2000-00-03
PRIOR PLING DATE: 2000-00-07
PRIOR PLING DATE: 2000-07-07
PRIOR PLING DATE: 2000-07
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Pred. No. 53;
0; Mismatches 6; Indels
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Burgess, Catherine E.
Casman, Stacke J.
Grosse, William M.
Gusev, Vladimir Y.
Ji, Weizhen
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Patturajan, Meera
Rastelli, Luca
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APPLICANT: Boldog, Ferenc L.
APPLICANT: Burgess, Catherine E.
                                                                                                          Shimkets, Richard A
Spaderna, Steven K.
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Liu, Xiaohong
Mezick, Amanda J.
                                                                                thenoy, Suresh G.
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Best Local Similarity 50.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Homo sapiens
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-10-190-115-114
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APPLICANT: ANGEROM, et al.

TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD FILE REFERENCE: 21402-589 B
CURRENT APPLICATION NUMBER: 00/898,994
PRIOR PLING DATE: 2001-07-03
PRIOR PAPLICATION NUMBER: 60/218,903
PRIOR PLING DATE: 2000-07-18
PRIOR PLING DATE: 2001-12-10
PRIOR APPLICATION NUMBER: 10/016,248
PRIOR FILING DATE: 2000-12-14
PRIOR PLING DATE: 2000-12-14
PRIOR PLING DATE: 2000-12-14
PRIOR PLING DATE: 2000-12-14
PRIOR PLING DATE: 2000-12-19
PRIOR PLING DATE: 2000-10-11
PRIOR PLING DATE: 2000-01-11
PRIOR PLING DATE: 2000-05-01
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      Gaps
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NUMBER OF SEQ ID NOS: 339
SOFTWARE: CuraSeqList version 0.1
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; OTHER INFORMATION: Description of Artifical Sequence: Domain
US-10-454-246-20
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      Indels
      9
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0; Mismatches
         Mismatches
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Publication No. US20030207394A1
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APPLICANT: Boldog, Ferenc L.
APPLICANT: Burgess, Catherine E.
APPLICANT: Casman, Stacie J.
APPLICANT: Grosse, William M.
APPLICANT: Grosse, William M.
APPLICANT: Grosse, Vladimir Y.
APPLICANT: Ji, Weizhen
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Sequence 20, Application US/10454246
Publication No. US20050053930A1
GENERAL INFORMATION:
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ORGANISM: Artificial Sequence
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Mezick, Amanda J
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Best Local Similarity 50.0
Matches 6; Conservative
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            6; Conservative
                                                                   6 WSXXXXCSXXCG 17
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US-10-190-115-111
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LENGTH: 397
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-190-115-116
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                                                                           APPLICANT: Spycek, Kimberly A.
APPLICANT: Spycek, Kimberly A.
APPLICANT: Spycek, Kimberly A.
APPLICANT: Szekeree, Edward S. Jr.
APPLICANT: Techernev, Velizar T.
APPLICANT: Techernev, Velizar T.
APPLICANT: Zerhusen, Bryan D.
APPLICANT: Zerhusen, Bryan D.
APPLICANT: Zerhusen, Bryan D.
APPLICANT: Zerhusen, Bryan D.
APPLICANT: Velizar T.
APPLICANT: Velizar C.
APPLICANT: Velizar C.
APPLICANT: Velizar D.
APPLICANT: Velizar C.
APPLICANT: Veliz
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Pred. No. 53;
0; Mismatches 6; Indels
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Publication No. US20030207394A1
GENERAL INFORMATION:
APPLICANT: Alsobrook, John P. II
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Alsobrook, John P. II
Boldog, Ferenc L.
Burgess, Catherine E.
Casman, Stacie J.
Grosse, William M.
Gusev, Vladimir Y.
Ji, Weizhen
Lepley, Denise M.
Liu, Xiaohong
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Padigaru, Muralidhara
Patturajan, Meera
                                   Shimkets, Richard A
Spaderna, Steven K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Shenoy, Suresh G.
Shimkets, Richard A
Spaderna, Steven K.
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Shenoy, Suresh G.
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Best Local Similarity 50.0
Matches 6; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                60 WSSWALCSTSCG 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-190-115-114.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT:
APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT:
APPLICANT:
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APPLICANT: Tchernev, Velizar T.
APPLICANT: Zerhusen, Bryan D.
APPLICANT: Zerhusen, Bryan D.
APPLICANT: Zerhusen, Bryan D.
TITE OF INVENTION: NOVEL ENCTEINS AND NUCLEIC ACIDS ENCODING SAME
FILE REPERSENCE: 21402-050 CTP
CURRENT PILING DATE: 2003-02-10
PRIOR APPLICATION NUMBER: 06/303,168
PRIOR APPLICATION NUMBER: 60/308,996
PRIOR PILING DATE: 2002-04-01
PRIOR FILING DATE: 2002-04-01
PRIOR FILING DATE: 2000-07-03
PRIOR PILING DATE: 2000-07-03
PRIOR PILING DATE: 2000-07-03
PRIOR PILING DATE: 2000-07-03
PRIOR APPLICATION NUMBER: 60/215,856
PRIOR PILING DATE: 2000-07-03
PRIOR PILING DATE: 2000-07-03
PRIOR PILING DATE: 2000-07-07
PRIOR APPLICATION NUMBER: 60/216,586
PRIOR PILING DATE: 2000-07-07
PRIOR PILING DATE: 2000-07-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 40; DB 15; Length 401;
Pred. No. 53;
0; Mismatches 6; Indels
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Best Local Similarity 50.0%;
Matches 6; Conservative (
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Search completed: April 1, 2005, 14:22:18 Job time : 114.348 secs

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Gaps

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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OM protein - protein search, using sw model

Run on:

April 1, 2005, 13:44:22; Search time 38.7391 Seconds (without alignments) 42.393 Million cell updates/sec

US-09-462-909D-9 59

1 XXXXXWSXXXXCSXXCGXXXXX 22 Title: Perfect score: Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

513545 Total number of hits satisfying chosen parameters:

513545 segs, 74649064 residues

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

Issued Patents AA:*

1: /cgiiz-6/ptodata/1/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		, Appli	, Appli	11, Appl	5426100	5426100	, Appli	, Appli	, Appli	6, Appl	4, Appl	, Appli	, Appli	, Appli	, Appli	2, Appl		20, Appl	, Appli	32422, A	47639, A	46823, A	58094, A	42783, A	5, Appl	Appli	, Appli	
	ion	5	u,	_			, 1	e H	ē	~	П	9	9	9	9	Н										e 7	9	
	Description	Sequence	Sequence	Sequence	Patent No.	Patent No	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Company
SUMMARIES		US-07-646-531D-5	US-08-488-273-5	US-09-197-770B-11	5426100-5	426100-5	US-08-985-526-1	PCT-US93-01652-1	US-08-985-526-3	US-09-854-845-16	US-09-854-845-14	US-09-854-845-6	US-09-854-845-2	US-09-854-845-8	09-854-845-4	US-09-854-845-12	US-09-854-845-10	US-08-313-288B-20	US-09-657-472-2	JS-09-270-767-32422	JS-09-270-767-47639	US-09-270-767-46823	US-09-270-767-58094	US-09-270-767-42783	9-369-364A-15	9-369-364A-7	US-07-646-531D-6	7.5-00-400-273-6
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	Query Match Length	23	53 1	23	23	23		239	441	939	954	1034	1049	1078	1093	1136	1151	1170	1170	120	120	479	677	847	874	997	23	23
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	Score	40	40	40	40	40	40	40	40	40	40	40	40	40	40	40	40	40	40	39	39	39	39	39	39	39	38	3.0
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ALIGNMENTS

Sequence 5, Application US/07646531D
Fatent No. 5200397
GENERAL INFORMATION:
APPLICANT: Deutch, Alan Howard
APPLICANT: Deutch, George Paul
TITLE OF INVENTION: Thrombospondin
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: W. R. Grace & Co.-Conn.
STREET: 7379 Route 32
CITY: Columny: Grace & Co.-Conn.
STREET: 7379 Route 32
CUNTRY: USA COMPUTER READABLE FORM:
MEDIUM TYPE: Flopyy disk
COMPUTER: IBM PC COMPALIDE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 5.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/646,531D
FILING DATE: 19910131
ATTORNEY/AGENT INFORMATION:
NAME: APPLICATION NUMBER: 33223
REGISTRATION NUMBER: 33223
REFERENCE/DOCKET NUMBER: 01-7896
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION STATEMENTON:
TELECOMMUNICATION FOR SEQ ID NO: 5: LENGTH: 23 amino acids TYPE: AMINO ACID SEQUENCE CHARACTERISTICS LENGTH: 23 amino acid TOPOLOGY: linear MOLECULE TYPE: peptide RESULT 1 US-07-646-531D-5 US-07-646-531D-5

Score 40; DB 1; Length (23; Pred. No. 5.4; 6; Indels Query Match 67.8%; Best Local Similarity 50.0%; Matches 6; Conservative

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Gaps

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4 WSEWTSCSTSCG 15 g

RESULT 2 US-08-488-273-5

COUNTRY:

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                                                                                                             LENGTH: 23
; TYPE: PRT
; GROANISM: Artificial Sequence
; PEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: fragment/ analog of thrombospondin
gs-09-197-770B-11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6; Indels
                                                                                                                                                                                                                                                                                                                   6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: DEUTCH, ALAN H.; TUSZYNSKI, GEORGE
APPLICANT: DEUTCH, ALAN H.; TUSZYNSKI, GEORGE
TITLE OF INVENTION: PIPTIDE FRAGMENTS AND ANALOGS OF
THROMBOSPONDIN
NUMBER OF SEQUENCES: 12
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/110,146
FILLING DATE: 20-UG-1993
FRICH APPLICATION DATA:
APPLICATION NUMBER: 896,527
FILLING DATE: 22-FEB-1990
FILLING DATE: 22-FEB-1990
                                                                                                                                                                                                                                                                         Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 6;
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Pred. No. 5.4;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Mismatches
CURRENT APPLICATION NUMBER: US/09/197,770B CURRENT FILING DATE: 1998-11-23 NUMBER OF SEQ ID NOS: 38 SEQ ID NO 11 LENGTH: 23 LENGTH: 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 40;
Pred. No. 5
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Best Local Similarity 50.0
Matches 6; Conservative
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Best Local Similarity 50.0
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5426100-5
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GENERAL INCENTATION:
APPLICANT: TUSTYNSKI, GEORGE
APPLICANT: Williams, Taffy
APPLICANT: Actor, Paul
TITLE OF INVENTION: REPROINVERSO POLYPEPTIDES THAT MIMIC OR INHIBIT
TITLE OF INVENTION: THROMBOSPONDIN ACTIVITY
FILE REFERENCE: 07206-0021
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
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             Sequence 5, Application US/08488273;
Patent No. 5840692
GENERAL INFORMATION:
APPLICANT: Deutch, Alan H.
TITLE OF INVENTION: THEOMOSPONDIN
TITLE OF INVENTION: THROMBOSPONDIN
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ANDRESS:
ADDRESSE: ADDRESS:
ADDRESSE: ADMITCH SCHWARZE JACOBS & NADEL, P.C.
STREET: 1601 Market Street, 36th Floor
                                                                                                                                                                                                                                                                                                        COMPUTEY: USA

ZIP: 19103-239

COMPUTER READABLE FORM:
MEDIUM TYPE: Ploppy disk:
COMPUTER: IBM PC Compatible
SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US 08/359,263
FILING DATE: 07-JUW-1995
CLASSIPICATION NUMBER: US 08/359,263
FILING DATE: 19-DEC-1994
PRIOR APPLICATION NUMBER: US 08/10,146
FILING DATE: 20-AUG-1993
PRIOR APPLICATION NUMBER: US 07/895,527
FRIING DATE: 20-AUG-1992
PRIOR APPLICATION NUMBER: US 07/483,527
FRIING DATE: 22-EB-1990
ATTORNEY/AGENT INFORMATION:
REGISTRATION NUMBER: 35-317
RELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
TELECTER: 3-3-404
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 40; DB 2
Pred. No. 5.4;
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Patent No. 6339062
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    67.8%;
50.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 23 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 50.0
Matches 6; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                     CITY: Philadelphia
STATE: Pennsylvania
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           amino acid
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US-09-197-770B-11
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US-08-488-273-5

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Gaps

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James A
CARRIER: DNA COMPLEXES CONTAINING DNA
ENCODING ANTI-ANGIOGENIC PEPTIDES AND THEIR USE IN GENE
THERAPY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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Pred. No. 31;
0; Mismatches 6; Indels
                                                                 OPERATING SYSTEM: PC-LUCS/MS-LUCS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/01652
FILING DATE: 19930222
CLASSITCATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/841,656
FILING DATE: 12-18-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/464,369
FILING DATE: 12-JAN-1990
ATTORNEY AGENT INFORMATION:
NAME: Fentress, Susan B.
REGISTRATION NUMBER: 3127
REFERENCE/DOCKET NUMBER: 92005-PCT
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/985,526
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    B: Connolly, Bove, Lodge, & Hutz
1220 Market Street, P.O. Box 2207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/608,845
FILING DATE: 16-JUL-1996
ATTORNEY/AGENT INFORMATION:
                  MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZIP: 19899
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
CMEDIUM TYPE: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 3, Application US/08985526 Patent No. 6080728
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: MCMORTOW Jr., ROBERT G
TELECOMMUNICATION INFORMATION:
TELEPHONE: (302) 658-9141
                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: (312)-456-7776
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 239 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  67.8%;
50.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 50.v-
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APPLICANT: MixBON, James
TITLE OF INVENTION: CARR
TITLE OF INVENTION: THER
NUMBER OF SEQUENCES: 43
CORRESPONDENCE ADDRESS:
ADDRESSEE: COMPOLLY, B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6 WSXXXXXCS 17
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PCT-US93-01652-1
  COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CITY: Wilmington STATE: Delaware
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRANDEDNESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-08-985-526-3
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                                                                                                                                 Sequence 1, Application US/08985526

Patent No. 6080728

GENERAL INFORMATION:
APPLICANT: Mixson, James A

TITLE OF INVENTION: CARRIER: DNA COMPLEXES CONTAINING DNA

TITLE OF INVENTION: THERAPY

TITLE OF INVENTION: THERAPY
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                                                                                                                                                                                                                                                                                                                                                 Sequence 1, Application PC/TUS9301652
GENERAL INFORMATION:
APPLICANT: Bouck, Noel P.
APPLICANT: Good, Deborah J.
APPLICANT: Frazier, William A.
TITLE OF INVENTION: Method and Composition for TITLE OF INVENTION: Inhibiting Angiogenesis NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3: Tilton, Fallon, Lungmus & Chestnut
100 South Wacker Drive, Suite 960
                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES: 43
CORRESPONDENCE ADDRESS:
ADDRESSEE: Connolly, Bove, Lodge, & Hutz
STREET: 1220 Market Street, P.O. Box 2207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pred. No. 29;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/608,845
FILING DATE: 16-ULL-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: MCMOLTOW Jr., Robert G
TELECOMMUNICATION INFORMATION:
TELEPAX: (302) 658-9141
TELEFAX: (302) 658-5613
INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        67.8%;
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Best Local Similarity 50.0
Matches 6; Conservative
6 WSXXXXCSXXCG 17
                                     4 WSEWTSCSTSCG 15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CITY: Chicago
STATE: Illinois
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ZIP: 60606-4002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 7
PCT-US93-01652-1
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                                                                                                RESULT 6
US-08-985-526-1
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APPLICANT: Wang, Xiaoming
APPLICANT: Wang, Xiaoming
APPLICANT: Wang, Xiaoming
APPLICANT: Wang, Xiaoming
APPLICANT: Scoville, John
APPLICANT: Truner, C. Alexander Jr.
TITLE OF INVENTION: No. 6750054el Human Semaphorin Homologs and Polynucleotides Encodigneral APPLICATION NUMBER: US (90) 6854, 845
CURRENT FILING DATE: 2001-05-14
PRIOR APPLICATION NUMBER: US 60/205, 274
PRIOR APPLICATION NUMBER: US 60/206, 893
PRIOR PILING DATE: 2000-06-02
NUMBER OF SEQ ID NOS: 50
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 6
LENGTH: 1034
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Walk, Name
APPLICANT: Walk, Name
APPLICANT: Walk, Name
APPLICANT: Wang, Xiaoming
APPLICANT: Soville, John
APPLICANT: Soville, John
APPLICANT: Soville, John
APPLICANT: Turner, C. Alexander Jr.
TITLE OF INVENTION: No. 6750054el Human Semaphorin Homologs and Polynucleotides Encodering APPLICATION NUMBER: US/09/854,845
CURRENT FILING DATE: 2001-05-14
PRIOR APPLICATION NUMBER: US 60/205,274
PRIOR APPLICATION NUMBER: US 60/205,274
PRIOR APPLICATION NUMBER: US 60/208,893
PRIOR FILING DATE: 2000-05-18
PRIOR FILING DATE: 2000-06-02
NUMBER OF SEQ ID NOS: 50
SOFTWARE: PastSEQ for Windows Version 4.0
SEQ ID NO 2
LENGTH: 1049
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Pred. No. 93;
0; Mismatches 6; Indels
                                                             DB 4; Length 954;
88;
                                                                                                                 6; Indels
                                                                  Score 40; DB 4
Pred. No. 88;
0; Mismatches
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                                                                                                                                                                                                                                                                                                                           Sequence 6, Application US/09854845
Patent No. 6750054
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50.0%;
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Best Local Similarity 50.0
Matches 6; Conservative
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                                                                                                                   Conservative
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US-09-854-845-6
; ORGANISM: homo sapiens
US-09-854-845-14
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Best Local Similarity
                                                                       Query Match
Best Local Similarity
Matches 6; Conserv
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APPLICANT: Walke, D. Wade

APPLICANT: Wang, Xiaoming

APPLICANT: Wang, Xiaoming

APPLICANT: Wang, Xiaoming

APPLICANT: Turner, C. Alexander Jr.

TITLE OF INVENTION: No. 6750054el Human Semaphorin Homologs and Polynucleotides Encod

TITLE OF INVENTION: NO. 6750054el Human Semaphorin Homologs and Polynucleotides Encod

TITLE OF INVENTION: NO. 6750054el Human Semaphorin Homologs and Polynucleotides Encod

TITLE OF INVENTION: NO. 675054el Human Semaphorin Homologs and Polynucleotides Encod

TITLE OF INVENTION NUMBER: US 60/205,274

PRIOR APPLICATION NUMBER: US 60/208,893

PRIOR PRILING DATE: 2000-06-02

NUMBER OF SEQ ID NOS: 50

NUMBER OF SEQ ID NOS: 50

SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Walke, D. Wade
APPLICANT: Walke, D. Wade
APPLICANT: Wang, Xiaoning
APPLICANT: Scoville, John
APPLICANT: Scoville, John
APPLICANT: Turner, C. Alexander Jr.
TITLE OF INVENTION: No. 675054el Human Semaphorin Homologs and Polynucleotides Encod
TITLE OF INVENTION: No. 675054el Human Semaphorin Homologs and Polynucleotides Encod
TITLE OF INVENTION: NO. 675074
FILE REFERENCE: LEX-017-05-14
PRIOR APPLICATION NUMBER: US 60/208,893
PRIOR APPLICATION NUMBER: US 60/208,893
PRIOR FILING DATE: 2000-06-02
NUMBER OF EGG ID NOS: 50
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 16-05-18
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Pred. No. 87;
0; Mismatches 6; Indels
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Pred. No. 49;
0; Mismatches 6; Indels
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Patent No. 6750054
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Patent No. 6750054
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50.0%;
                                                                                                                                                                                                  67.8%;
    TELEFAX: (302) 658-5613
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 441 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 50.00
Best Local 6; Conservative
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Best Local Similarity 50.0
Matches 6; Conservative
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US-09-854-845-16
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US-09-854-845-14
                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 9
US-09-854-845-16
                                                                                                                                                      US-08-985-526-3
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Gaps ö

6; Indels

Mismatches

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6; Conservative

Matches

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GENERAL INFORMATION:

APPLICANT: Walke, D. Wade

APPLICANT: Wane, Xiaoming

APPLICANT: Wane, Xiaoming

APPLICANT: Scorille, John

APPLICANT: Scorille, John

APPLICANT: Turner, C. Alexander Jr.

TITLE OF INVENTION: NO. 6750054el Human Semaphorin Homologs and Polynucleotides Encodi

FILE REFERENCE: LEX-0177-USA

CURRENT APPLICATION NUMBER: US/09/854,845

CURRENT APPLICATION NUMBER: US 60/205,274

PRIOR APPLICATION NUMBER: US 60/208,893

PRIOR PILING DATE: 2000-05-18

PRIOR PILING DATE: 2000-06-02

NUMBER OF SEQ ID NOS: 50

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO: 20
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Pred. No. 1e+02
0; Mismatches
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                                          Sequence 12, Application US/09854845
Patent No. 6750054
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Best Local Similarity 50.0%;
Matches 6; Conservative
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ORGANISM: homo sapiens
                      JS-09-854-845-12
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                                                                                                                                                                                                                                  APPLICANT: Walke, D. Wade
APPLICANT: Walke, D. Wade
APPLICANT: Wang, Xiaoming
APPLICANT: Wang, Xiaoming
APPLICANT: Wang, Xiaoming
APPLICANT: Scoville, John
APPLICANT: Turner, C. Alexander Jr.
TITLE OF INVENTION: No. 6750054e1 Human Semaphorin Homologs and Polynucleotides Encod
CURRENT APPLICATION NUMBER: US, 609, 854, 845
CURRENT APPLICATION NUMBER: US, 60/205, 274
PRIOR APPLICATION NUMBER: US, 60/205, 274
PRIOR APPLICATION NUMBER: US, 60/208, 893
PRIOR FILING DATE: 2000-06-02
NUMBER OF SEQ ID NOS: 50
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
APPLICANT: Walke, D. Wade
APPLICANT: Wang, Xiaoming
APPLICANT: Scovilla.
APPLICANT: Scovilla.
Turner, C. Alexander Jr.
TITLE OF INVENTION: No. 6750054el Human Semaphorin Homologs and Polynucleotides Encor
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Pred. No. 96;
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CURRENT FILING DATE: 2001-05-14
PRIOR APPLICATION NUMBER: US 60/205,274
PRIOR PLING DATE: 2000-05-18
PRIOR PLING DATE: 2000-06-05
PRIOR PLING DATE: 2000-06-05
NUMBER OF SEQ ID NOS: 50
SOFTWARE: FASTSEQ for Windows Version 4.0
                                                                                                                                                               Sequence 8, Application US/09854845 Patent No. 6750054 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 14
US-09-854-865-4
; Sequence 4, Application US/09854845
; Patent No. 6750054
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Best Local Similarity 50.0°
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                                               568 WSSWALCSTSCG 579
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Matches 6; Conservative
6 WSXXXXXCSXXCG 17
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LENGTH: 1078
TYPE: PRT
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LENGTH: 1093
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Gaps

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DB 4; Length 1136; le+02; 6; Indels

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GenCore version 5.1.6 Copyright (c) 1993 - 2005 Compugen Ltd.

- protein search, using sw model OM protein

April 1, 2005, 13:22:55 ; Search time 153.522 Seconds (without alignments) 55.424 Million cell updates/sec Run on:

US-09-462-909D-9 59 Perfect score:

1 XXXXXXXXXXXXXXXXXX 22 Sequence:

Gapop 10.0 , Gapext 0.5 **BLOSUM62** Scoring table:

2105692 Total number of hits satisfying chosen parameters:

2105692 seqs, 386760381 residues

Searched:

Minimum DB E Maximum DB E

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Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

geneseqp2000s:* geneseqp2001s:* geneseqp2002s:* geneseqp2003as:* geneseqp2003bs:* geneseqp2003bs:* A Geneseq 16Dec04:* geneseqp1990s:*geneseqp1990s:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

					SUMMARIES		
Result No.	Score	Query Match	o Query Match Length DB	DB	ID	Description	
	40	67.8	23	0	AAR13629	Aarlagod Thromboon	
~	40	67.8	23	N	AAW81482	-	
3	40	67.8	23	ß	AAE20746	-	
4	40	67.8	23	œ	ADM80537	-	
<u>د</u>	40	67.8	20	~	AAY49503	-	
	40	67.8	20	4	AAB50005	•	
7	40	67.8	143	4	ABB11084	Abb11084 Human sec	
80	40	67.8	157	m	AAB08133	Aab08133 Amino aci	
0	40	67.8	170	œ	ADL70644	Adl70644 Human thr	
10	40	67.8	183	Ŋ	AAU74791	Aau74791 Human thr	
11	40	67.8	218	~	AAW40287	Aaw40287 Human TSP	
12	40	67.8	218	~	AAY06182	Aay06182 Thrombosp	
13	40	67.8	239	7	AAR40823	Aar40823 Human thr	
14	40	67.8		œ	ADP04871	Adp04871 Sea squir	
15	40	67.8		œ	ADJ34131		
16	40	67.8		7	ADD18225	Add18225 Human mol	
17	40	67.8		7	ADD18230	Human	
18	40	67.8		7	ADD18228	Add18228 Human mol	
19	40	67.8			ADD18232	Add18232 Human mol	
20	40	67.8	-	œ	ADJ34125	Adj34125 Human sec	
21	40	67.8		8	ADJ34123	Adj34123 Human sec	
- 22	40	67.8		ω	ADJ34121	Adj34121 Human sec	
23	40	67.8	·	00	ADJ34127	Adj34127 Human sec	
24	40	67.8	432	80	ADQ39359	Adq39359 Human myo	
25	40	67.8	432	8	ADQ39357	Add39357 Human mvo	

Aay06183 Thrombosp Aay06183 Thrombosp Aau02916 Angiotens Aab4602 Human can Aau02915 Angiotens Adu02914 Angiotens Adu02914 Angiotens Abg94994 Babesia a Adp04709 Sea squir Aau02913 Angiotens Aag68295 Human sem Aay64990 Human see Aag68291 Human see Aag68291 Human see Aag68291 Human see	Human Human Human Human Human
AAW40288 AAV06183 AAU02916 AAU02915 AAU02914 ADN02474 AAU02914 AAU02913 AAC68296 AAG68295 AAG68295 AAG68295 AAG68291	AAG6292 ABG34077 ADA01364 ADA43793 ADA43561
4 4 4 4 4 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	078 092 092 6 092 6
677.88 677.88 677.88 677.88 677.88 677.88	67.8 67.8 67.8 1 67.8 1 67.8
4 4 4 4 4 4 4 4 4 4 4 4 4 4 4	
0.000000000000000000000000000000000000	44444 12444

ALIGNMENTS

Antiviral agent; wound healing; platelet aggregation; thrombotic; Ą. AAR13629 standard; peptide; 23 90US-00483527. 91US-00646531. 91EP-00101908 Thrombospondin peptide p11. (revised)
(first entry) thrombolytic. 11-PEB-1991; 31-JAN-1991; 22-FEB-1990; 25-MAR-2003 31-OCT-1991 28-AUG-1991. EP443404-A. Synthetic. AAR13629; RESULT 1 AAR13629

(GRAC) GRACE & CO-CONN W R. (MEDI-) MED COLLEGE OF PENNSYLVA. (DEUT/) DEUTCH A H.

Deutch AH, Tuszynski GP;

WPI; 1991-254044/35.

New peptide fragments and analogues of thrombospondin - useful for inhibiting tumour metastasis, as clotting agents and to promote or inhibit cell adhesion and immune modulation.

Claim 3; Page 26; 30pp; English

The peptide is a synthetic fragment of human thrombospondin and is based on the sequence motif of Robson et al (Nature (1988) 335.79-82). It has thrombospondin-like activity and can be used: (1) to inhibit tumour cell metastasis and atherosclerosis; (2) to promote or nhibit platelet aggregation, angiogenic activity, thrombotic or thrombolytic activity, immune modulaton and cell adhesion; (3) to promote wound healing; and (4) as an antiviral aggent (interferes with cell adhesion). The peptide is prepd. by std. synthesis techniques. See also AAR13626-R13641. (Updated on 25-MAR-2003 to correct PA field.)

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                                               ö
                                                  Gapa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Method for mimicking or inhibiting thrombospondin activity - using thrombospondin peptides.
                                                                                                                                                                                                                                                                                                      Thrombospondin; thrombin sensitive protein; TSP; cell-adhesion; micoganic activity; chemotactic; haemostatic; tumour; microbial; parasite; metastasis; platelet aggregation; fibrinolytic; malaria; immune modulation; wound healing; atherosclerosis; angiogenesis; complement modulator; diagnostic reagent.
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                 Score 40; DB 2; Length 23;
                                                Indels
                                                                                                                                                                                                                                                                                 Thrombospondin synthetic analog compound p11.
                                                     0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           UNIV ALLEGHENY HEALTH SCI.
                                                                                                                                                                                         AAW81482 standard; peptide; 23 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 3; Col 29; 19pp; English.
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92US-00896527.
93US-00110146.
94US-00359263.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     95US-00488273.
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                          67.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Tuszynski GP;
                                                                                                                                                                                                                                                          (first entry)
                                          Local Similarity 50.0
                                                                                    WSXXXXCSXXCG 17
                                                                                                                   WSEWTSCSTSCG 15
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Sequence 23 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        07-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   19-DEC-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     22-FEB-1990;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    09-JUN-1992
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                                                                                                                                                                                                                                                                                                                                                                                                                Synthetic.
                                                                                                                                                                                                                              . AAW81482;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (UYAL-)
                             Query Match
                                                                                                                                                                    RESULT 2
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DB 2; Length 23;

67.8%; Score 40;

Query Match

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The invention relates to a polypeptide having the retroinverso form of a polypeptide that minics or inhibits the biological activity of thrombospondin (Thrombin sensitive peptide (TSP), or a retroinverso thrombospondin (Thrombin sensitive peptide (TSP), or a retroinverso polypeptide in which cysteine residues are modified with a sulphydryl blocking group. The polypeptide is useful for inhibiting the invasive and metastasis, invasion, adhesion and for inhibiting the invasive and metastatic activity of melanoma cells. The polypeptides are also useful for promoting and inhibiting cellular attachment to tissue culture flasks for anti-platelet aggregation and antimalarial activity, as diagnostic for anti-platelet aggregation and antimalarial activity, as diagnostic consequents in different therapeutic applications, in cancer therapy, for reagents in different therapeutic opplications, in cancer therapy, for transports and thrombotycopenia continuous antherapeutic applications, atherosclerosis, angiogenesis, complement modulators, and antimetastatic agents, in biomedical devices, complement modulators, and antimetastatic agents, in biomedical devices, complement modulators, and antimetastatic agents, in biomedical devices, complement modulators, and antimetastatic agents in biomedical devices, complement modulators, and antimetastatic purposes, and content of the corresponding requence is TSP peptide. Note: This sequence is solate thrombospondin cells for diagnostic or therapeutic purposes, and content sequence coll membranes. The present sequence is TSP peptide. Note: This sequence content the corresponding sequence found in column 11-12 does not conserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Novel polypeptide having retroinverso form of polypeptide that mimics/inhibits biological activity of thrombospondin, for treating cancer, malaria, wound healing, atherosclerosis, angiogenesis, thrombotic
                                                                                                                                                                                                                                                                                                                                                 Thrombospondin; TSP; thrombin sensitive peptide; wound healing; cancer; angiogenesis; tumour cell metastasis; anti-platelet aggregation; therapy; malaria; thrombotic condition; atherosclerosis; rheumatoid arthritis; vulnerary; sickle cell disease; thrombocytopaenia; diabetic retinopathy; cytostatic; protozoacide; haemostatic.
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               Gaps
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50.0%; Pred. No. 11;
ive 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Tuszynski G, Actor
                                                                                                                                                                                                        AAE20746 standard; peptide; 23 AA.
                                                                                                                                                                                                                                                                                                                             Thrombospondin (TSP) peptide #13.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             98US-00197770.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      98US-00197770.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (INKI-) INKINE PHARM CO INC.
                                                                                                                                                                                                                                                                                            (first entry)
                     Conservative
                                                                 6 WSXXXXCSXXCG 17
                                                                                                      4 WSEWTSCSTSCG 15
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  Best Local Similarity
Matches 6; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Unidentified.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               23-NOV-1998;
                                                                                                                                                                                                                                                                                            01-JUL-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Williams T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15-JAN-2002.
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                                                                                                                                                                                                                                                     AAE20746;
                                                                                                                                                                           RESULT 3
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Human; METH1; METH2; anti-angiogenic; metalloprotease thrombospondin; cancer; diagnosis; hyperproliferative disorder; autoimmune disease; angiogenesis inhibitor; abnormal wound healing; inflammation; rheumatoid arthritis; psoriasis; endometrial bleeding disorder; diabetic retinopathy; macula degeneration; haemangioma; detection; arterial-venous malformation; immune deficiency.
    Human METH1 thombospondin-like domain #1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 50 AA;
                                                                                                                                                                                                                      Homo sapiens.
                                                                                                                                                                                                                                                                WO9937660-A1
                                                                                                                                                                                                                                                                                                                                                          22-JAN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                      23-JAN-1998;
28-AUG-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention relates to a polypeptide which has the retroinverso form of a polypeptide which mimics or inhibits the biological activity of thrombospondin. Also described is a method for inhibiting cell metastasis, invasion or adhesion, comprising administering to a host the retroinverso polypeptide compound. The retroinverso polypeptide is useful for inhibiting tumour cell metastasis, invasion or adhesion, for promoting wound healing or implant acceptance, or for treating malaria, atherosclerosis or thrombosis. The present sequence represents a thrombospondin analogue of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New retroinverso polypeptide, useful for inhibiting tumor cell metastasis, invasion or adhesion, for promoting wound healing or implant acceptance, or for treating malaria, atherosclerosis or thrombosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  thrombospondin; tumour cell metastasis; cell invasion; cell adhesion; wound healing; implant acceptance; malaria; atherosclerosis; thrombosis.
                                                     Gaps
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    DB 5; Length 23;
                                                   6; Indels
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Score 40; DB 5
Pred. No. 11;
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                      Thrombospondin analogue peptide #11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Williams T, Tuszynski G, Actor P;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (INKI-) INKINE PHARM MCP HAHNEMANN.
                                                                                                                                                                                                                                                             ADM80537 standard; peptide; 23 AA.
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50.0%;
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    67.8%;
                        50.0%;
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                                                6; Conservative
                                                                                            6 WSXXXXCSXXCG 17
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 23 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Synthetic.
                                                                                                                                                                                                                                                                                                           ADM80537;
    Query Match
                                                Matches
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metalloprotease thrombospondin (METH) proteins METH1 and METH2
metalloprotease thrombospondin (METH) proteins METH1 and METH2
cespecitively. METH1 and METH2 have been found to be potent inhibitors of angiogenesis both in vitro and in vivo. They can be used for treating cancer and other disorders related to angiogenesis including abnormal wound healing, inflammation, rheumatoid arthritis, psoriasis, endometrial bleeding disorders, diabetic retinopathy, some forms of macula degeneration, haemangiomas, and arterial-venous malformations. They may be useful in treating deficiencies or disorders of the immune system, by cativating or inhibiting the proliferation, differentiation, or mobilisation (chemotaxis) of immune cells. The etiology of these immune deficiencies or disorders may be genetic, somatic, such as cancer or some deficiencies or disorders may be genetic, somatic, such as cancer or some cutoimmune disorders, acquired (e.g. by chemotherapy or toxins), or infectious. They can also be used to treat inflammatory conditions, both chronic and acute conditions. The products can also be used for detection and diagnosis. AAZ32002 to AAZ32080, and AAY49503 to AAX49511 represent
                                                                                                                                                                                                                                                                                                                                                                                                                  New isolated metalloprotease thrombospondin polypeptides, useful for treating hyperproliferative disorders, cancers or autoimmune disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human; METH; metalloprotease; thrombospondin; angiogenesis inhibition;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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Pred. No. 20;
0; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                        Ruben SM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure, Fig 5; 457pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAB50005 standard; protein; 50 AA.
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99WO-US001313.
                                                         98US-0072298P.
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50.0%;
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                                                                                                                                                           (IRUE/) IRUELA-ARISPE
                                                                                                                                                                                   (HAST/) HASTINGS G A. (RUBE/) RUBEN S M.
                                                                                                                                                                                                                                                                                                                                                        WPI; 1999-590684/50.
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AAY49503 standard; protein; 50 AA.

10-JAN-2000 (first entry)

AAY49503;

RESULT 5
AAY49503
ID AAY4
XX
AC AAY4
XX
AC AAY4
XX
DT 10-J

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Human; cytokine; cell proliferation; cell differentiation; growth factor; haematopoiesis regulation; tissue growth; immunomodulator; activin;

Human secreted protein homologue, SEQ ID NO:1454.

(first entry)

11-JAN-2002

ABB11084;

ABB11084 standard; peptide; 143 AA.

RESULT 7

ABB11084

haematopolesis regulation, tissue growth, immunomodulator; glowin haddon inhibin, chemotaxis, tissue growth, immunomodulator; glowin; inhibin, chemotaxis, chemokinesis; thrombolysis; oncogenesis; proliferation; metastasis; cancer; tumour; haematopoletic disorder; proliferation arthritis; chronic inflammatory condition; proliferative retinopathy; atherosclerosis; ocronary heart disease; arterial ischaemia; tissue regeneration; wound healing; infection; immune disorder; cell culture; drug screening; gene therapy; antiniflammatory; cell culture; drug screening; gene therapy; antiniflammatory; cytostatic; osteopathic; vasculatic; cardiant; virucide; antibacterial; antibacterial; antifungal; vulnerary; antiulcer.

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The present invention relates to human METH1 and METH2, (WE for metalloprotease and TH for thrombospondin; see AAB50002 and AAB50003).

The present sequence is a TSP domain which are found in METH protein. The present sequence is a TSP domain which are found in METH protein. The used for inhibiting angiogenesis in an individual, and for treating cancer, benign tumours, an ocular angiogenic disease, rheumatoid arthritis, psoriasis, delayed wound healing, endometriosis, arthritis, psoriasis, hypertrophic scars, nonunion fractures, vasculogenesis, granulations, hypertrophic scars, nonunion fractures, coronary collaterals, crebral collaterals, arteriovenous malformations, coronary collaterals, crebral collaterals, arteriovenous malformations, coronary collaterals, crebral collaterals, arteriovenous malformations, is necvascularisation, telangicetasia, haemophiliac joints, angiofibroma, fibromuscular dysplasia, wound granulation, Crohn's disease or therosclerosis. METH can also be used in birth control. METH can also be used in diagnostic methods for the prognosis of cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   METH1 and METH2 polynucleotides and encoded polypeptides, used to inhibit angiogensis in the treatment of disorders such as cancer, rheumatoid
cancer therapy, benign tumour; ocular angiogenic disease; rheumatoid arthritis; psoriasis; wound healing; endometriosis; vasculogenesis; granulation; hypertrophic scar; nonunion fracture; sclenderma; trachoma; vascular adhesion; myocardial angiogenesis; coronary collateral; cerebral collateral; arteriovenous malformation; ischaemic limb angiogenesis; osler webber syndrome; TSP domain; plaque neovascularisation; telangiectasia; heemophiliac joint; angiofibroma; fibromuscular dysplasia; wound granulation; Crohn's disease; atherosclerosis; birth control.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Trulli SH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ruben SM, Jonak ZL,
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BETH ISRAEL DEACONESS MEDICAL CENT.
IRUELA-ARISPE L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure; Fig 5; 768pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Iruela-Arispe L, Hastings GA,
Fornwald JA, Terrett JA;
                                                                                                                                                                                                                                                                                                                                                            99US-0144882P.
99US-0147823P.
99US-00373658.
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22-FEB-2000; 2000US-0183792P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HUMAN GENOME SCI INC.
                                                                                                                                                                                                                                                                                                          25-MAY-2000; 2000WO-US014462
                                                                                                                                                                                                                                                                                                                                          99US-00318208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  arthritis and psoriasis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RUBEN S M.
JONAK Z L.
TRULLI S H.
FORNWALD J A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HASTINGS G A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2001-025136/03.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TERR/) TERRETT J A.
                                                                                                                                                                                                                                   WO200071577-A1.
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                                                                                                                                                                                                     Homo sapiens.
                                                                                                                                                                                                                                                                                                                                              25-MAY-1999;
                                                                                                                                                                                                                                                                         30-NOV-2000.
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                                                                                                                                                                                                                                                                                                                                                                                   10-AUG-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (IRUE/)
(HAST/)
(RUBE/)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HUMA-)
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(BETH-)
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Sequences ABB10981-ABB12330 represent 1350 novel human polypeptides, and sequences ABA08225-ABA09574 represent nucleic acids encoding them. The invention also relates to vectors and recombinant host cells comprising a invention also relates to vectors and recombinant host cells comprising a nucleotide of the invention, methods of producing the nucleotides of polypeptides in a sample, and methods of identifying compounds which bind to polypeptides of the invention. Although novel, many of the polypeptides of the invention have homology to known proteins, thereby compounds of the invention have homology to known proteins, thereby potential therapeutic applications. The polypeptides of the invention may potential therapeutic applications. The polypeptides of the invention may insight into their probable biological activities, and hence contavities are acidities, including cytokine, cell proliferation or cell differentiation activities; stem cell growth factor activity; is sequentially activity; activity activity; activity activity, activity, activity, activity, activity, activity, activity, activity, activity, activities, nemocatic or chemokinetic activities, haemostatic, thromboic or may be considered in oncogenesis, cancer cell proliferation or metastasis.

The invention are useful for preventing, treating or ameliorating medical cancers, haematopoletic disorders (e.g., myeloid or lymphoid call cancers, haematopoletic disorders (e.g., myeloid or lymphoid call cancers, haematopoletic or chemokars), conditions, e.g., by protein or gene therapy. Such conditions and annormal arterial ischaemia, bone disorders (e.g., osteoporosis), and abnormal arterial ischaemia, bone disorders (e.g., osteoporosis), and abnormal arterial ischaemia, bone disorders (e.g., osteoporosis), and abnormal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human proteins and DNA encoding sequences useful for preventing, treating or ameliorating a medical condition in a mammalian subject e.g. arthritis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 20; Page 144; 1963pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               03-FEB-2000; 2000US-00496914.
27-APR-2000; 2000US-00560875.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            05-FEB-2001; 2001WO-US003800.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (HYSE-) HYSEQ INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Liu C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N-PSDB; ABA08328.
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                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          09-AUG-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          and cancer.
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Gaps

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Indels

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0; Mismatches

Score 40; Pred. No. 2

67.8%;

6; Conservative 6 WSXXXXCSXXCG 17 7 WSEWTSCSTSCG 18

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Query Match Best Local Similarity Matches 6; Conserv

Sequence 50 AA;

DB 4; Length 50;

proteins are used for the treatment of conditions associated with

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healing (e.g., of burns, incisions and ulcers), while those with mimunomodulatory activities may be used in the treatment of viral, bacterial and fungal infections in addition to immune disorders. Polypeptides with growth factor activity may be used in cell cultures to promote cell growth. For example, such polypeptides may be used to manipulate stem cells in culture to give rise to neuroepthelial cells that can be used to augment or replace cells damaged by illness, autoimmune disease or accidental damage. The polypeptides and nucleotides may also be used in the diagnosis of the above conditions, and in drug screening techniques. The present sequence represents a novel human
repair (or nucleic acids encoding them) may be used to promote wound healing (e.g., of burns, incisions and ulcare)
                                                                                                                                                                                                                                                                                                                                                         polypeptide of the invention
                      888888888888888
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Sequence 143 AA;

Gaps ö 4; Length 143; 6; Indels Score 40; DB 4 Pred. No. 45; 0; Mismatches 67.8%; Local Similarity 50.0 6 WSXXXXCSXXCG 17 Query Match Matches ઠે

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89 WSSWALCSTSCG 100

RESULT 8

AAB08133 standard; protein; 157 AA. AAB08133; Amino acid sequence of hTSP-1 Type I repeat peptide (TRP).

(first entry)

04-DEC-2000

Type 1 repeat, thrombospondin-1; TSP-1; Type I repeat peptide; TRP; KIAA0688; KIAA0550; angiogenesis inhibitory protein; angiogenesis; cancer; tumour; rheumatorid arthritis; psoriasis; retinopathy; coular angiogenic disease; macular degeneration; corneal graft rejection; neovascular glaucoma; retrolental fibroplasia; rubeosis; Osler-Webber Syndrome; myocardial angiogenesis; haemophiliac joint; plaque neovascularisation; telanqisctasia; nagiofibroma; wound granulation; coronary collateral; cerebral collateral; arteriovenous malformation; ischemic limb angiogenesis; neovascular glaucoma; retrolental fibroplasia; fracture; vasculogenesis; heliobacter related disease; hematopoiesis; ovulation; menstruation; placentation; birth control; embryo implantation.

Homo sapiens

WO200047622-A2

17-AUG-2000

15-FEB-2000; 2000WO-GB000520

99GB-00003408. 15-FEB-1999; (OXFO-) OXFORD BIOMEDICA UK LTD

Martin-Rendon E, Kingsman SM; Mazarakis N,

WPI; 2000-549137/50.

Non-naturally occurring Type I repeat peptide (TRP) derived from human thrombospondin-1, KIAA0688 or KIAA0550 proteins, useful in the treatment of anglogenesis and/or cancer.

Claim 4; Fig 2; 84pp; English

The present sequence represents the amino acid of human thrombospondin-1 (hTSP-1) Type I repeat peptide (TRP). The specification describes a non-naturally occurring TRP, derived from hTSP-1, KIAA0688 or KIAA0550 proteins. The TRP protein is an angiogenesis inhibitory protein. TRP

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               angiogenesis and cancer. Angiogenic mediated diseases include tumours, rheumatoid arthritis, psoriasis, ocular angiogenic diseases, retinopathy of prematurity, macular degeneration, corneal graft rejection, neovascular glaucoma, retrolental fibroplasia, rubbosis), Osler-Webber Syndrome, myocardial angiogenesis, plaque neovascularisation, telangiectasia, haemophiliac joints, angiofibroma, wound granulation, coronary collaterals, cerebral collaterals, arteriovenous malformations, ischemic limb angiogenesis, neovascular glaucoma, retrolental fibroplasia, heliobacter related diseases, fractures, vasculogenesis, hematopoiesis, ownlation, menstruation and placentation. TRPs are also useful in the treatment of disease of excessive or abnormal stimulation of endothelial cells. TRP can also be used as a birth control agent, as it prevents the vascularisation required for embryo implantation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New purified thrombospondin fragment extracted from a body fluid, useful for diagnosing cancer e.g. adenoma, adenocarcinoma, carcinoma, lymphoma or leukemia or as calibrators, indicators, immunogens and analytes.
                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                                                                                                                                                                                                           Score 40; DB 3; Length 157;
Pred. No. 48;
0; Mismatches 6; Indele
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human; thrombospondin-1; epitope; cancer; diagnosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human thrombospondin-1 domain of type 1 repeats.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure; SEQ ID NO 43; 76pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADL70644 standard; protein; 170 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                20-AUG-2003; 2003WO-US026023.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        23-AUG-2002; 2002US-0405494P.
21-APR-2003; 2003US-00419462.
                                                                                                                                                                                                                                                                                                                                                                       67.8%;
50.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                 6; Conservative
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                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
Matches 6; Conserv
                                                                                                                                                                                                                                                                                                                              Sequence 157 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADL70644;
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using the difference between (1) and (2) as a quantitation of the amount of TSP fragment or portion. Suitable epitopes are provided ADI/0602-
CC ADI/0638 Detection or quantification of the TSP fragment or portion is performed in order to detect the presence, or monitor the course, of a general defaultie, accurated insease, classase or condition selected from cancer, renal failure, renal disease, disease or expire dermatitie, vacculitie, renal dislure, renal disease, dispease or condition selected from cancer, renal failure, renal disease, classes mellitus, waccardial infarterion, liver disease, splenectomy, dispease mellitus, myocardial infarterion, liver disease, splenectomy, dermatory at the monocus, Kawasaki syndrome, non-specific vasculitie, juvenile thouse exphematosus, Kawasaki syndrome, non-specific vasculitie, juvenile rheumatoid arthritis, vasculitie, syndrome, Henochtheus distribution, a condition associated with flotting, a condition associated with flotting, a condition associated with flotting, a condition associated with consumption of platelet activation, a condition associated with consumption of condition associated with endothelial activation, a condition associated with sold and or release of thrombospondin and/or a thrombospondin condition associated with endothelial activation, an antibiotic craction, an aspartame reaction, atopic dermatitis, eczem, reaction, an aspartame reaction, atopic dermatitis, eczem, craction, and aspartame reaction, atopic dermatitis, eczem, craction, associated with a cryoglobulin, and a condition associated with a cryoglobulin, and a crock with a cryoglobulin, and a cryoglobulin, and cryoglobulin, and cryoglobulin, and cryoglobulin, and cryoglobulin, and
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Score 40; DB 8; Length 170; Pred. No. 51; 0; Mismatches 6; Indels 67.8%; Query Match
Best Local Similarity 50...
Best Local Similarity 50... 6 WSXXXXCSXXCG 17 7 WSEWTSCSTSCG 18 Sequence 170 AA; 셤 à

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AAU74791 standard; protein; 183 AA. 09-APR-2002 (first entry) AAU74791; RESULT 10 AAU74791

Human thrombospondin-1 (TSP-1) derived recombinant protein, 3TSR.

Thrombospondin-1; TSP-1; cytostatic; angiogenesis; vasotropic; vulnerary; neovascularisation; cell proliferation inhibitor; cancer; solid tumour; haemangioma; acoustic neuromas; neurofibroma; trachoma; trachoma; pyogenic granulomas; rheumatoid arthritis; ocular angiogenic disease; retinopathy; psoriasis; macular degeneration; corneal graft rejection; neovascular glaucoma; retrolental fibroplasia; rebeosis; angiofibroma; osler-Webber syndrome; myocardial angiogenesis; haemophiliac joints; plaque neovascularisation; telangiectasia; wound granulation; apoptosis; mutant; mutein; 3TSR,

Homo sapiens. Synthetic.

Key Peptide

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/label= Vector_derived_peptide Location/Qualifiers

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The invention describes a composition comprising cDNA encoding fragments of human thrombospondin-1 (TSP -1), a type 1 repeat polypeptide and cof human thrombospondin-1 (TSP -1), a type 1 repeat polypeptide and cof human thrombospondin-1 (TSP -1), a type 1 repeat polypeptide and cofferent polypeptide and content of tumour (inhibiting necvascularisation in the tumour); for decreasing proliferation of tumour cells; in the tumour, in the property of diseases and conditions associated with angiogenic activity treatment of diseases and conditions associated with angiogenic activity creatment of diseases and conditions associated with angiogenic activity creatment of diseases and conditions and pyogenic granulomas), acoustic neuromas, neurofibromas, trachomas, and pyogenic granulomas), acoustic neuromas, neurofibromas, trachomas, and pyogenic granulomas), created arthritis, psoriasis, ocular angiogenic diseases (e.g. rheumatoid arthritis, psoriasis, ocular angiogenic diseases (e.g. rheumatoid arthritis, psoriasis, ocular angiogenic diseases (e.g. corneal graft rejection, neovascular glaucoma, retrolental fibroplasias, corneal graft rejection, neovascular glaucoma, retrolental fibroplasias, corneal graft rejection, neovascular glaucoma, retrolental fibroplasias, corneal graft rejection, neovascular saction, haemophiliac joints, telangiectasia, plaque neovascularisation; the composition in the tumour cells. This amino acid sequence inhibits neovascularisation in the tumour cells. This sagions of TSP-1, (TSP-1) and containing the 3 type 1 repeat (TSR) regions of TSP-1, appear in the specification but has been created using the human thrombospondin-1 (TSP-1) wild type sequence (see AAU74771) from thrombospondin-1 (TSP-1) wild type sequence (see AAU74771) from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
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                                                                                                                                                                                                                                                                                                                                                                                  Composition useful for treatment of cancer comprises cDNA encoding amino acids of human thrombospondin-1 or its conservative variant and a
6. .175
/note= "Residues 361-530 of human thrombospondin-1 (TSP-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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                                                                      /label= Vector_derived_peptide
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Pred. No. 54;
0; Mismatches
                                                                                                                                                                                                                                                                      (BETH-) BETH ISRAEL DEACONESS MEDICAL CENT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAW40287 standard; protein; 218 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Example 1; Page; 54pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 67.8%;
50.0%;
                                                                                                                                                                                             25-MAY-2001; 2001WO-US017250.
                                                                                                                                                                                                                                  26-MAY-2000; 2000US-0207994P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              18-AUG-1998 (first entry)
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Best Local Similarity 50.v
6; Conservative
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                                                        176. .183
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 183 AA;
                                                                                                                  WO200191781-A2
                                                                                                                                                            16-DEC-2001
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                                                                                                                                                                                                                                                                                                                    Lawler JW;
                                                                                                                                                                                                                                                                                                                                                                                                                                          carrier
  Protein
                                                            Peptide
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This sequence represents an anti-angiogenic fragment of the thrombospondin I protein. The invention provides a carrier:DNA complex that comprises DNA (see ANXS8725-42) coding for an anti-angiogenic protein or peptide, the complex being deliverable to the site of a tumour in vivo, and which additionally comprises regulatory elements for expressing the anti-angiogenic DNA in a tumour or tumour vasculature. The complex may also include DNA encoding a tumour suppressor protein, especially p53. The carrier is a liposome, cationic polymer, micelle, microsphere, virus, viral component, or a combination of these, and administration is by intravenous or intratumoral injection. The complexes are useful in gene therapy for inhibition of tumour growth. The types of tumors which may be treated include solid tumors such as melanomas and tumors in the lung, colon, brain and breast
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      hTSP-1; platelet glycoprotein; angiogenesis; neovascularisation; inhibitor; solid tumour; skin cancer; angiogenic dysfunction; melanoma; diabetic retinopathy; psoriasis; neovascular glaucoma; Kaposi's sarcoma; inflammation; retrolental fibroplasia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         . 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 40; DB 2;
Pred. No. 62;
0; Mismatches
                                                                                        GAA"
                                                                                                                                        5000
              "encoded by CTC"
                                                             by AAC"
                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; Page 17-18; 46pp; English.
                                                                                                                                                                                                                                                                                                                                                          Inhibition of growth of solid tumors.
                                      "encoded by
                                                                                                               β
                                                                                      "encoded by
                                                                                                                                       "encoded by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAR40823 standard; protein; 239 AA.
                                                               "encoded
                                                                                                                                                                                                                                           97US-00985526
                                                                                                                                                                                                                  98EP-00100135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              67.8%;
50.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (revised)
(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  17
                                                               /note=
177
               'note=
                                                                                                                                          /note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human thrombospondin 1.
                                                                                        'note=
                                       'note=
                                                                                                                 'note=
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         85 WSEWTSCSTSCG
                                                                                                                                                                                                                                                                                                                     WPI; 1999-315406/27.
  Misc-difference 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                 N-PSDB; AAX58725
                                                Misc-difference
                                                                                                  Misc-difference
                                                                                                                          Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 218 AA;
                          Misc-difference
                                                                         Misc-difference
                                                                                                                                                                                                                                                                   NOSXIW (/SXIW)
                                                                                                                                                                                                                  07-JAN-1998;
                                                                                                                                                                                                                                           05-DEC-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         25-MAR-2003
03-MAR-1994
                                                                                                                                                                EP921193-A1
                                                                                                                                                                                         09-JUN-1999
                                                                                                                                                                                                                                                                                             Mixson AJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAR40823;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 13
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   셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This sequence represents the thrombospondin gene TSP1 which is used in a method to produce a cationic vehicle consisting of a cationic liposome:DNA complex where the DNA encodes an anti-angiogenic peptide or tumour suppressor protein. Such complexes are used for treatment of neoplastic and metabolic diseases especially for gene therapy of tumours
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Anti-angiogenic; carrier:DNA complex; tumour; gene therapy; human; thrombospondin I; melanoma; lung cancer; colon cancer; brain cancer;
                                                                                                                                                                                                                                                                                                                                                                                            Complexes of DNA encoding anti-angiogenic peptide - with cationic liposome(s) or cationic polymer, useful for, e.g. gene therapy of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 40; DB 2; Length 218;
Pred. No. 62;
0; Mismatches 6; Indels
                                                                                                                                      199. .217
/label= anti-angiogenic peptide
                                                                        /label= anti-angiogenic peptide
                                                                                    142. .159
/label= anti-angiogenic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note= "encoded by CGG"
                                                                                                                         note= "encoded by CGG
                                                                                                                                                                           /note= "encoded by CT"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
                                                cocation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAY06182 standard; protein; 218 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 9; Page 6; 47pp; English
                                                                                                                                                                                                                                                      97EP-00112154
                                                                                                                                                                                                                                                                               96US-00680845
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       67.8%;
metabolic disease; tumour
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  16-AUG-1999 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Thrombospondin I fragment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6 WSXXXXCSXXCG 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   85 WSEWTSCSTSCG 96
                                                                                                                                                                                                                                                                                                                                                        WPI; 1998-078839/08.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Key
Misc-difference 160
                                                                                                                                                                                                                                                                                                      (MIXS/) MIXSON A J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                    N-PSDB; AAV10493
                                                                                                             Misc-difference
                                                                                                                                                             Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 218 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              breast cancer.
                          Homo sapiens
                                                                                                                                                                                                                                                      16-JUL-1997;
                                                                                                                                                                                                                                                                             16-JUL-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
                                                                                                                                                                                                    EP819758-A2
                                                                                                                                                                                                                             21-JAN-1998
                                                                                                                                                                                                                                                                                                                               Mixson AJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAY06182;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                         tumours.
                                                           Peptide
                                                                                    Peptide
                                                                                                                                    Peptide
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Gaps

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Length 218; Indels

Gaps

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This invention relates to novel genes and the encoded proteins thereof that are derived from the sea squirt Ciona intestinalis. Specifically, it refers to those genes that are expressed in the tissues or organs of the sea squirt during its developmental phase. The present invention of development and hence for developing regeneration of the mechanism of development and hence for developing regeneration of the mechanism of development and hence for developing regeneration of the mechanism of development and hence for developing regeneration of the research of various genetic diseases, as well as the analysis of cell the research of various genetic diseases, as well as the analysis of cell compositions can be useful for environmental measurements and water surveys, particularly for sea water surveys, and also for the preparation contrastormed sea squirt for improving edibility of sea squirt such as the contrastormed sea squirt protein sequence that has tissue specific expression during development, given in exemplification of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human; NOVX; secreted protein; cancer; diabetes; obesity; endocrine disorder; gene therapy.
                                                                                                                                                                                                                                                                                                                      Score 40; DB 8; Length 324;
Pred. No. 85;
0; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Burgess CE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADJ34131 standard; protein; 397 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2002US-0390006P.
2002US-0396706P.
2002US-0402832P.
2002US-0403486P.
2002US-0403522P.
2002US-0403748P.
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2002US-038702P.
2002US-0387540P.
2002US-0387559P.
2002US-0387934P.
2002US-0389723P.
2002US-0389723P.
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2002US-0386041P.
2002US-0386453P.
2002US-0386974P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2002US-0387037P.
2003US-00454246:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               04-JUN-2003; 2003WO-US017512.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human secreted protein NOV2h
                                                                                                                                                                                                                                                                                                                               67.8%;
                                                                                                                                                                                                                                                                                                                                            50.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Anderson DW, Boldog FL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                 6 WSXXXXCSXXCG 17
                                                                                                                                                                                                                                                                                                                                                                                                                                  85 WSSWSRCSSSCG 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (CURA-) CURAGEN CORP.
                                                                                                                                                                                                                                                                                                                                            Local Similarity
tes 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO2004000997-A2
                                                                                                                                                                                                                                                                                                Sequence 324 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           07-JUN-2002;
10-JUN-2002;
11-JUN-2002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         03-JUN-2003;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        19-MAR-2002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              07-JUN-2002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                12-JUN-2002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                13-JUN-2002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .7-JUN-2002;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15-AUG-2002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            06-JUN-2002;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADJ34131;
                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADJ3413
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                      Certain fragments of thrombospondin, a glycoprotein found in the alpha granules of platelets, can inhibit vascularisation. Peptides derived from the hTSP sequence are useful for inhibiting necosacularisation, esp. in solid tumnours such as melanomas. The inhibitory peptides can also be used in other diseases involving analogenic dysfunction. See AAR40824-R40830. (Updated on 25-WAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sea squirt protein with tissue specific expression in development Seq466.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            sea squirt; regeneration medicine; gene therapy; cell proliferation;
differentiation; reproduction; environmental measurement; water survey.
                                                                                                                                                                                                                                                                                                  Compsn. for inhibiting angiogensis - contg. a vascularisation inhibitor comprising a peptide capable of inhibiting vascularisation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Novel gene cluster which is specifically expressed in tissue or organ during developmental phase of sea squirt, useful for elucidation of mechanism of development of tissue or organ of sea squirt.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gapa
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 40; DB 2; Length 239;
Pred. No. 67;
0; Mismatches 6; Indels
                                                                                                                                                                                                                                         Frazier WA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 1; SEQ ID NO 466; 1846pp; Japanese
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN.
                                                                                                                                                                                                                                                                                                                                                              Claim 10; Page 41-42; 51pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADP04871 standard; protein; 324 AA.
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                                                                                                                                                                                                                                         Good
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         67.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                31-JUL-2002; 2002JP-00222593
                                                                                                                                     93WO-US001652
                                                                                                                                                                       92US-00841656
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                      (NOUN ) UNIV NORTHWESTERN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6 WSXXXXXXXXX 17
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                                                                                                                                                                                                                                         Bouck NP, Polverini PJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2004-287079/27.
N-PSDB; ADP04870.
                                                                                                                                                                                                                                                                          WPI; 1993-288118/36.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ciona intestinalis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 239 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           JP2004057129-A.
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                                                                                                                                     22-FEB-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              26-FEB-2004
                                                                                                                                                                        24-FEB-1992;
                                      Ното варіеля
                                                                     WO9316716-A1
                                                                                                    02-SEP-1993
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Matches

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ADP0487.

X S X X B X

Edinger SR;

Casman SJ,

Stone DJ; Zhong M; Gusev VY, Ji W; , Padigaru M; Gorman L, Guo X, Gusev VY
Millet I, Ort T, Padiga
M. Peyman JA, Rieger DK;
J. Smithson G, Spytek KA,
NM, Voss EZ, Zerhusen BD, ,, Ellerman K, Gerlach VI, Gor Macdougall JR, Malyankar UM, M SK, Patturajan M, Pena CEA, erg ME, Sciore P, Shenoy SG, RJ, Tchernev VT, Vernet CAM, Prayaga SK, Pa Rothenberg ME, **Taupier RJ**,

WPI; 2004-082483/08 N-PSDB; ADJ34130 New isolated NOVX polypeptides useful for treating, preventing and diagnosing pathological conditions with NOVX-associated disorders, such as cancer, obesity, diabetes and inflammatory or CNS diseases.

Claim 1; SEQ ID NO 20; 418pp; English

The invention relates to a new isolated polypeptide (designated NOVX) comprising one of 141 fully defined sequences, their mature forms, a protein comprising one or more conservative substitutions or having at least 954 identity to one of the 141 proteins. Also included are a composition comprising NOVX (or a NOVX nucleic acid molecule (NA)), a kit comprising the composition of NOVX nucleic acid molecule encoding a NOVX protein, producing NOVX (comprising nucleic acid molecule encoding a NOVX protein, producing NOVX (comprising outleic acid molecule encoding a NOVX protein, producing NOVX (comprising nucleic acid molecule encoding a NOVX identifying a potential comprises a vector comprising NOVX NA), identifying an agent that binds to NOVX, identifying a potential comprise or physpeptide, where the call comprises a vector comprising that is related for a modulator of activity of or latency or predisposition to a pathology associated with NOVX, treating a pathology associated with NOVX nucleic acid molecule, a cell comprising the vector, an antibody that immunospecifically binds to composition in a sample, and determining the presence of or predisposition or to a disease associated with altered levels of expression of NOVX or the molecule in a sample, and determining the presence of or predisposition or to a disease associated with altered levels of expression of activity of treatment of disorders associated with aberrant expression or activity of the NOVX polypoptole, such as cancer, diabetes, obestty, and endocrine, concerning assays, chromosome mapping, tissue typing, gene contents and predictive medicine. The present sequence represents a NOVX polypoptole. protein

Sequence 397 AA;

ö 67.8%; Score 40; DB 8; Length 397; 50.0%; Pred. No. 1e+02; tive 0; Mismatches 6; Indels Query Match
Best Local Similarity 50.0
Matches 6; Conservative

ö

Gaps

6 WSXXXXCSXXCG 17

à

58 WSSWALCSTSCG 69

1, 2005, 13:54:27 Search completed: April Job time: 154.522 secs

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GenCore version 5.1.6 Copyright (c) 1993 - 2005 Compugen Ltd.

- protein search, using sw model OM protein April 1, 2005, 13:24:31 ; Search time 75.6522 Seconds (without alignments) 81.226 Million cell updates/sec Run on:

US-09-462-909D-8 fitle:
Perfect score:

1 WSGWSSCSRSCG 12 Sequence: BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

1612378 seqs, 512079187 residues Searched:

Total number of hits satisfying chosen parameters:

seq length: 0 seq length: 200000000 Minimum DB Maximum DB

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

UniProt 03:*
: uniprot sprot:*
: uniprot trembl:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

anopheles g homo sapien caenorhabdi mus musculu rattus norv cryptospori xenopus lae mus musculu bos taurus drosophila homo sapien ciona intes mus musculu mus musculu drosophila caenorhabdi caenorhabdi caenorhabdi caenorhabdi cryptospori bos taurus drosophila plasmodium taurus Description 099221 066048 066048 066889 068889 07229 07229 076510 091465 091894 O6p7j9 Q86pq3 Q966k7 Q8t3a0 Q8cg65 Q700k0 P59509 Q8te57 P98167 Q8ms£8 ATS7 HUMAN Q19204 AT19 MOUSE AT16_HUMAN SSPO BOVIN 076510 Q9TTS5 Q8MRL5 Q7Z291 Q7Z291 Q81U50 Q9W493 Q6P7J9 Q86PQ3 Q966K7 Q8MSF8 Q9VKV3 Q9GZ21 Q6 PCK8 Q6 PD18 Q8MYA8 Q6 BSA9 Q9XSV8 Query Match Length DB 1361 1461 1641 125 238 685 685 867 1020 1020 1059 1686 257 1089 2098 3869 100.0 Score Result

Q9upz6 homo sapien Q69zu6 mus musculu Q7rf52 plasmodium Q69hl7 ciona intes Q42113 brachydanio Q8te60 homo sapien Q8b4s1 mus musculu Q694r5 homo sapien Q81vu0 homo sapien P55114 caenorhabdi Q42114 brachydanio Q22580 caenorhabdi Q82580 caenorhabdi Q8k206 mus musculu Q8k206 mus musculu
Q9UPZ6 Q69ZU6 Q7RF52 Q69LL7 Q42113 AT18 HUMAN Q8BKA1 Q6P4R5 Q81VU0 YVD3 CAEEL Q22580 Q8KZ06 Q8KZ06
0000000000000
1502 1668 2401 504 808 1092 1221 129 551 872 900
811.8 811.8 81.8 80.5 800.5 799.2 799.2 799.2
6622223333665244444444444444444444444444
₩₩₩₩₩₩₩₩₩₩₩₩₩₩₩₩₩₩₩₩₩₩₩₩₩₩₩₩₩₩₩₩₩₩₩₩₩

ALIGNMENTS

a collaboration the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch). This SWISS-PROT entry is copyright. It is produced through a collaboratic between the Swiss Institute of Bioinformatics and the EMBL outstation Lamalle D., Dastugue B., Meiniel A.; "SCO-spondin family secreted by the subcommissural organ is a candidate in the modulation of neuronal Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovinae; Bos. -i- SIMILARITY: Belongs to the thrombospondin family.
-i- SIMILARITY: Contains at least 2 EGF-like domains.
-i- SIMILARITY: Contains at least 1 F5/8 type C domain.
-i- SIMILARITY: Contains at least 3 LDL-receptor class A domains.
-i- SIMILARITY: Contains at least 4 TSP type-1 domains.
-i- SIMILARITY: Contains 1 VWFC domain. SEQUENCE FROM N.A.
TISSUE=Ependymocyte;
MEDLINE=96338614; PubMed=8743952;
Gobron S., Monnerie H., Meiniel R., Creveaux I., Lehmann W., 01-0CT-1996 (Rel. 34, Created) 01-0CT-1996 (Rel. 34, Last sequence update) 29-MAR-2004 (Rel. 43, Last annotation update) 867 AA PRT; STANDARD; SCO-spondin (Fragment). Bos taurus (Bovine). NCBI_TaxID=9913; aggregation."; SSPO BOVIN P98167; Bovinae;

FAS8 C. Gal Dind like. LDL receptor A. PMP_SGCI. Cysrich_TIL. EMBL; X93922; CAA63815.1; -. nterPro; IPR000884; TSPI InterPro; IPR002919; InterPro; IPR000421; nterPro; IPR002172; nterPro; IPR009041;

Pfam; PF00754; F5 F8 type C; 1. Pfam; PF00057; Ldl_recept_a; 3.

homo sapien

of

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"Subcommissural organ/Reissner's fiber complex: characterization SCO-spondin, a glycoprotein with potent activity on neurite outgrowth.";
Glia 32:177-191(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 77; DB 2; Length 5146;
Pred. No. 0.058;
; Mismatches 0; Indels 0
MEDLINE=20465125; Pubmed=11008217;
DOI=10.1002/1098-1136(200011)32:2<177::AID-GLIA70>3.0.CO;2-V;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            50184; VWFC_2; 2.
5146 AA; 543588 MW; 724C5FB8727E13DA CRC64;
                                                                                                                                                                                                                          Meiniel A.;
Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: Contains 1 P5/8 type C domain.
EMBL; AJ416457; CAC94914.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                    HSSP, P98162; IKTB.
GO; GO:0005576; C:extracellular; IEA.
GO; GO:0005179; Fibramone activity; IEA.
GO; GO:001414; F:procease inhibitor activity; IEA.
GO; GO:0007155; P:cell adhesion; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT; 4998 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROSITE, PS00261; GLYCC HORMONE BETA_1; PROSITE; PS01209; LDLRA_1; 7. PROSITE; PSS0068; LDLRA_2; 9.
                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR002919; Cysrich Til.
InterPro; IPR004207; Cysrich Til.
InterPro; IPR01489; EMI.
InterPro; IPR00421; FA58 C.
InterPro; IPR00145; Gly. hormoneB.
InterPro; IPR00172; iDi. receptor A.
InterPro; IPR008037; prot inh.PMP.
InterPro; IPR001007; WP.C.
InterPro; IPR001007; WWF.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PROSITE; PSO1225; CTCK 2; 1.
PROSITE; PSO1286; PASSC 1; UNKNOWN 1.
PROSITE; PSO1286; FASSC 2; 1.
PROSITE; PSS0022; FASSC 3; 1.
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PROSITE; PS01208; VWPC 1; UNKNOWN 1.
PROSITE; PS50184; VWPC 2; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pfam; PP07546; EMI; 1.
Pfam; PP00754; FS PB type_C; 1.
Pfam; PP00757; Ld_recept a; 10.
Pfam; PP05375; PacIfastin_I; 1.
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(TrEMBLrel. 23, I
(TrEMBLrel. 26, I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pfan; PP01826; TIL; 10.
Pfan; PP00090; TSP 1; 25.
Pfan; PP00093; VWC; 1.
Pfan; PP00094; VWD; 3.
PRINTS; PR00261; LDLRECEPTOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.08;
                                                                                                                                                                                 SEQUENCE FROM N.A.
TISSUE-Subcommissural organ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2485 WSGWSSCSRSCG 2496
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FA58C; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SMART; SM00068; GHB; 1.
SMART; SM0192; LDLa; 10
SMART; SM00209; TSP1; 25
SMART; SM00214; VWC; 3.
SMART; SM00214; VWC; 3.
PROSITE; PS01225; CTCK_2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SMART; SM00041;
SMART; SM00231;
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01-MAR-2003 (
01-MAR-2004 (
                                                    Gobron S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         08CG65
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ID O8
AC O8
DT 01
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                                                PRINTS; PR00261; LDLRECEPTOR.
PRINTS; PR01706; TSPIREPEAT.
PROSITE; PS01285; PASSC_1; 1.
PROSITE; PS01286; PASSC_2; 1.
PROSITE; PS01209; LDLRA_1; 3.
PROSITE; PS0009; LDLRA_1; 3.
PROSITE; PS50089; IDLRA_2; 3.
PROSITE; PS50089; TSP1; 4.
PROSITE; PS50184; VWFC_2; 1.
Calcium-binding; Cell adhesion; EGF-like domain; Glycoprotein; Repeat.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Name=sco-spondin;
Bos taurus (Bovine).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovinae; Bos.
NCBI_TaxID=9913;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   linked (GlCNAc. . .) (Potential)
-linked (GlCNAc. . .) (Potential)
-linked (GlCNAc. . .) (Potential)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length (867;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        91817 MW; 9538F2108E787B49 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  LDL-receptor class A 1.
LDL-receptor class A 2.
LDL-receptor class A 3.
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Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%; Score 77; DB 1; 100.0%; Pred. No. 0.012;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TSP type-1 3.
TSP type-1 4.
By similarity.
                                                                                                                                                                                                                                                                                                                        TSP type-1 1.
EGF-like 1.
EGF-like 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Mismatches
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VWFC.
                                                                                                                                                                                                                                                                                                                                                                                                                                     F5/8 type C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-UTN-2002 (TYENBLrel. 21, Created) 01-UTN-2002 (TYENBLrel. 21, Last seq 01-MAR-2004 (TYENBLrel. 26, Last ann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
TISSUE=Subcommissural organ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     767 WSGWSSCSRSCG 778
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 100.
Best Local Similarity 100.
Matches 12; Conservative
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                                         Pfam; PF00090; TSP_1; 4.
Pfam; PF00093; VWC; 1.
                       Pfam; PF01826; TIL; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        867 88;
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Gaps

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Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORFNames=CG6232;
Drosophila melanogaster (Fruit fly).
Eukaryota; Metanogaster Arthropods; Hexapoda; Insecta; Pterygota;
Neopeera; Endopterygota; Diptera; Brachycera; Muscomorpha;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 2; Length 5141;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PROSITE; PS50092; TSP1, 24.
PROSITE; PS01208; VWFC_1; UNKNOWN_1.
PROSITE; PS501184; VWFC_2; 2.
SEQUENCE 5141 AA; 550644 MW; 1772AE67F02CA5E3 CRC64;
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Last annotation update)
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Last annotation update)
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PROSITE; PSS0120; EXE_3; 1.
PROSITE; PS01209; LDLRA_1; 8.
PROSITE; PS01209; LDLRA_1; 8.
PROSITE; PSS0068; LDLRA_2; 10.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 73; DB 2
Pred. No. 0.21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR000421; FA58 C.
InterPro; IPR001545; Gly_hormoneB.
InterPro; IPR00172; LDL_receptor_A.
InterPro; IPR000884; TSPI.
InterPro; IPR00552; VWC_out.
InterPro; IPR001007; VWF_C.
InterPro; IPR001846; VWF_D.
                                                                                                                                                                                                                                                                                                                                                   GO, GO:0007155; P:cell adhesion; IEA. GO; GO:0007155; P:cell adhesion; IEA. InterPro; IPR0022919; Cysrich TIL. InterPro; IPR006209; Cys. Knot. C. InterPro; IPR006209; EGF. Like. InterPro; IPR011489; EMI.
         Created)
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PROSITE; PS01186; EGF 2; UNKNOWN 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pfam; PF00090; TSP 1; 25.
Pfam; PF00093; VWC; 1.
Pfam; PF00094; VWC; 1.
PRINTS; PR0024; LDLRECEPTOR.
SWART; SW00192; LDLA; 10.
SWART; SW00219; TSP1; 25.
SWART; SW00219; VWC out; 9.
SWART; SW00216; VWC out; 9.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        94.8%;
91.7%;
      05-JUL-2004 (TrEMBLrel. 27, 05-JUL-2004 (TrEMBLrel. 27, 05-JUL-2004 (TrEMBLrel. 27,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-OCT-2002 (TrEMBLrel. 22, 01-OCT-2002 (TrEMBLrel. 22, 01-MAR-2004 (TrEMBLrel. 26,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2491 WSGWSDCSRSCG 2502
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Best Local Similarity 91.7
Matches 11, Conservative
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                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                        Name=sco-spondin;
                                                                                                                                                                            NCBI_TaxID=10116;
                                                                    SCO-spondin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GM15606p.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   QBMSF
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                                                                                                                                                                        Gencalves N., Simon-Chazottes D., Creveaux I., Meiniel A., Gencalves N., Simon-Chazottes D., Creveaux I., Meiniel A., Guenet J-L., Meiniel R.; Guenet J-L., Meiniel R.; Brownes SCO-spondin, a gene of the thrombospondin type 1 repeat (TSR) superfamily expressed in the brain."; Gene 312:263-270(2003).

-I- SIMILARITY: Contains 1 F5/8 type C domain.

HSSP; P01130; 1AJJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
Name-Scospondin; Synonyms-sco-spondin;
Mam musculus (Mouse).
Eukaryots; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 94.8%; Score 73; DB 2; Length 4998; 91.7%; Pred. No. 0.2; ive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4998 AA; 535028 MW; DA2ABABDA47DF225 CRC64;
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PROSITE; PS01186; EGF 7; 2.
PROSITE; PS0022; PA58C 3; 1.
PROSITE; PS00261; GLYCO HORMONE BETA 1; UNKNOWN 2.
PROSITE; PS01209; LDLRA 1; 8.
PROSITE; PS0068; LDLRA 2; 10.
PROSITE; PS00089; TSP1; 25.
PROSITE; PS00092; TSP1; 25.
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SWART; SM00209; GHB; 1.
SWART; SM00192; LDLa; 10.
SWART; SM00209; TSP1; 25.
SWART; SM00216; VWC; 4.
SWART; SM00216; VWD; 2.
PROSITE; PS00196; COPPER_BLUE; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                         MGD, MGI:2674311; Scospondin.
GO; GO:0005737; C:cytoplasm; IC.
InterPro; IPR00923; BlueCu 1.
InterPro; IPR002919; Cysrich TIL.
InterPro; IPR006209; EGF_like.
InterPro; IPR01499; EMI_
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR000421; PASB C.
InterPro; IPR001545; Gly_hormoneB.
InterPro; IPR002172; LDL_receptor_
InterPro; IPR008037; Prot_inh_PMP.
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Ldl recept a; 10.
Pacifastin I; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR008085; TSP 1.
InterPro; IPR001007; VWF_C.
InterPro; IPR001846; VWF_D.
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nes 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 WSGWSSCSRSCG 12
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SEQUENCE 4998 AA; 5
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                                                                                                                                                        SEQUENCE FROM N.A.
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PRINTS; PR01705;
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fam;

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Gaps

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Query Match

Matches

8 g D 0700K0 0700K0;

RESULT 4 Q700K0 ID Q7001 AC Q7001

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Lewis S.E.;
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                                                       Stapleton M., Brostein P., Hong L., Agbayani A., Carlson J.,
Champe M., Chavez C., Dorsett V., Dresnek D., Farfan D., Frise E.,
Champe M., Chavez C., Dorsett V., Dresnek D., Farfan D., Frise E.,
Champe M., Chavez C., Dorsett V., Dresnek D., Farfan D., Frise E.,
Chamilde A., Mungall C.J., Nunco J., Pacleb J., Park S.,
Celniker S., Phouanenavong S., Wan K., Yu C., Lewis S.E., Rubin G.M.,
Celniker S.; Orn-2002) to the EMBL/GenBank/DDBJ databases.
EMBL, AY11849; AMM50709.1; --
RESP, PO7996; LLSL.
RISP; PO7996; LLSL.
RISP; PO7996; LLSL.
RISP; PO7996; LLSL.
RIPBARG. FBGH0032222.
RIPBARG. FRGH00909; PLAC.
RIPBARG. FRGH00909; PLAC.
RIPBARG. FRGH009099; PLAC.
RIPBARG. FRGH009099; PLAC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
NCBI_TaxID=7227;
                                                                                                                                                                                                                                                                                                                                                         Score 70; DB 2; Length 880;
Pred. No. 0.12;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                 880 AA; 98882 MW; FB3FA4D5B54106CE CRC64;
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Last sequence update)
Last annotation update)
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Ephydroidea; Drosophilidae; Drosophila.
NCBI_TaxID=7227;
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                                                                                                                                                                                                                                                           Pfam; PF05986; ADAM spacerl; 1. Pfam; PF00090; TSP 1; 3. SMART; SM00209; TSP1; 6. PROSTTE; PS550900; PLAC; 1. PROSTTE; PS50900; TSP1; 5.
                                                                                                                                                                                                                                                                                                                                                               90.9%;
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01-OCT-2002 (TrEMBLrel. 22,
01-MAR-2004 (TrEMBLrel. 26,
                                                                                                                                                                                                                                                                                                                                                                                                                                                        185 WSDWSSCSRSCG 196
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Matches 11, Conservative
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                                                                                                                                                                                                                                                                                                                                      SEQUENCE
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Q9VKV3
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Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri, Reses M.G.,
Reinert K., Remington K., Saunders R.D., Scheeler F., Shen H.,
Shue B.C., Siden-Kiamos I., Simpson M., Stupski M.P., Smith T.,
A Syirskas K., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
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Mang Z.Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
Milliams S.M., Woodager, Worley K.C., Wu D., Yang S., Yao Q.A., Ye J.,
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A The genome sequence of Drosophila melanogaster.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDILINE=22426070; PubMed=12537573; MEDILINE=22426070; PubMed=12537573; Kaminker J.S., Bergman C.M., Kronmiller B., Carlson J., Svirskas R., Patel S., Fites E., Mheeler D.A., Lewis S.E., Rubin G.M., Ashburner M., Celniker S.E., "The transposable elements of the Drosophila melanogaster euchromatin: "The transposable elements of the Drosophila melanogaster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE-22426065.

Celniker S.E., Wheeler D.A., Kronmiller B., Carlson J.W., Halpern A., Celniker S.E., Wheeler D.A., Kronmiller B., Carlson J.W., Halpern A., Patel S., Adams M., Champe M., Dugan S.P., Frise B., Hodgson A., George R.A., Hoskins M.A., Laverty T., Muzny D.M., Nelson C.R., Pacieb J.M., Park S., Pfeiffer B.D., Richards S., Sodergren E.J., Pacieb J.M., Park S., Pfeiffer B.D., Richards S., Sodergren E.J., Wainston R., Stuton G.G., Venter Weinstock G., Scherer S.E., Myers E.W., Gibbs R.A., Rubin G.M.; Weinstock G., Scherer S.E., Myers E.W., Gibbs R.A., Rubin G.M.; Pinishing a whole-genome shotgun: Release 3 of the Drosophila melanogaster euchromatic genome sequence."; Genome Biol. 3:RESEARCH0079-RESEARCH0079 (2002).
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MEDLINE=22426069; PubMed=12537572;
Mista S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
Mista S., Crosby M.A., Kaminker J.S., Millburn G.H., Prochnik S.E.,
Smith C.D., Tupy J.L., Whitfied B.J., Bayraktaroglu L., Berman B.P.,
Bettencourt B.R., Celniker S.E., de Grey A.D., Drysdale R.A.,
Bratris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
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EMBL, AE003628; AAF52956.3; --
FlyBase; FBgn0032252; CG6232.
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Genome Biol. 3:RESEARCH0083-RESEARCH0083(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           a genomics perspective.";
Genome Biol. 3:RESEARCH0084-RESEARCH0084 (2002).
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Pred. No. 0.12;
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InterPro; IPR010909; PLAC.
InterPro; IPR000884; TSP1.
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91.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Science 287:2185-2195(2000).
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PROSITE; PS50092; TSP1; 3.
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ses 11; Conserv
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797 WSGWSSCSRDC 807
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Klein S., Strausberg
Submitted (OCT-2003)
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Mus musculus (Mouse).
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                                                                                                                                                                                                 SEQUENCE FROM N.A.
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Klauener R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh P.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapheton M.J., Boraldo M.F., Casavant T.L., Scheetz T.E.,
Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Frange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Villalon D.K., Muzny D.W., Sodergren E.J., Lu X., Gibbs R.A.,
Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE-20189602; PubMed=10930736; MEDLINE-20189602; PubMed=10930736; PubMed=2028-Diaz S., Amar C., McLauchlin J.; Pentaza-Diaz S., Amar C., McLauchlin J.; Pentaza-Diaz S., Amar C., McLauchlin J.; Penta identification and characterisation of an unusual genotype of Cryptosporidium from human faeces as Cryptosporidium meleagridis."; PEMB, Microbiol. Lett. 189:189-194 (2000). HSSP; P07996; 1LSL. ARG01095.1; -.. HSSP; P07996; 1LSL. InterPro; 1PR000884; TSP1. PEmBL; PR000896; TSP1; 3. PR00151TE; PS50092; TSP1; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MGC68835 protein.
Xenopus laevis (African clawed frog).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
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MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        87.0%; Score 67; DB 2; Length 168; 83.3%; Pred. No. 0.07;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2; Indels
                                                                                                                                                                                                                                                                                                                          Eukaryota, Alveolata, Apicomplexa, Coccidia, Eimeriida,
Cryptosporidiidae, Cryptosporidium.
NCBI_TaxID=93969;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CE9516EEE86479C3 CRC64;
                                                                                                                                                                                                                 01-MAR-2001 (TrEMBLrel. 16, Last sequence update) 01-MAR-2004 (TrEMBLrel. 26, Last annotation update) Thrombospondin-related adhesive protein (Fragment).
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05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
                                                                                                                                                    168 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT; 1088 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Mismatches
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                                                                                                                                                                                                 Created)
                                                                                                                                                 PRT;
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                                                                                                                                                                                                                                                                                                          Cryptosporidium meleagridis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            05-JUL-2004 (TrEMBLrel. 27, 05-JUL-2004 (TrEMBLrel. 27,
                           185 WSDWSSCSRSCG 196
1 WSGWSSCSRSCG 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 WSGWSSCSRSCG 12
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                                                                                                                                                    PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      85 WSGWSDCSTSCG 96
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NCBI_TaxID=8355;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                   Name=TRAP-C1
                                                                                                                                                                                          01-MAR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
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                                                                                                    RESULT 7
Q9GZ21
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COPCK8
COPCC
AC GOPC
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Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
Krzywinski M.I., Skalaka U., Smailus D.E., Schnerch A., Schein J.E.,
Jones S.J., Marra M.A.;
"Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                               TISSUE=Embryo;
MEDILNE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;
Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
Richardson P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Genetic and genomic tools for Xenopus research: The NIH Xenopus
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Pred. No. 0.36;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       122657 MW; 4DFCD371A7CD8176 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (OCT-2003) to the EMBL/GenBank/DDBJ databases.
EMBL, BC059288; AAH59288.1; -.
GO; GO:0016020; C:membrane; IRA.
GO; GO:0004872; F:receptor activity; IRA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
                                                                                                                                                                           and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
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InterPro; IPR003659; Plexin-like.
InterPro; IPR003659; Plexin-like.
InterPro; IPR001657; Sema.
InterPro; IPR00884; TSP1.
InterPro; IPR008085; TSP1.
InterPro; IPR008085; TSP1.
Ffam; PF01403; Sema; 1.
Pfam; PF00090; TSP1; 5.
PRINTS; PR01705; TSP1; 5.
PRINTS; PR01705; TSP1; 5.
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STRAIN=C57BL/6; TISSUE=Brain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Dev. Dyn. 225:384-391(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           87.0%;
90.9%;
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SMART; SM00630; Sema; 1.
SMART; SM00209; TSP1; 6.
PROSITE; PS50092; TSP1; 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity 90.9
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us-09-462-909d-8.rup

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Query Match
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                    none;
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Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Frange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
Richards S., Worley R.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Villalon D.K., Muzuy D.M., Sodergren B.J., Lu X., Gibbs R.A.,
Rahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
Miting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Blakesley R.W., Touchman J.W., Green B.D., Dickson M.C.,
Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
Rrzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
Jones S.J., Marra M.A.;
T. "Generation and initial analysis of more than 15,000 full-length human
"I proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
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Caenorhabditida; Rhabditida; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
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83.3%; Pred. No. 0.44;
ive 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE 1361 AA; 149549 MW; 49D04B6A28AFA877 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Strausberg R.; Submitted (OCT-2003) to the EMBL/GenBank/DDBJ databases. EMBL; BC058991; AAH58991.1; -. HSSP; P15167; 1ATL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HSEP; PISSET; 1ATL.

100, GO:0004222; F:metalloendopeptidase activity; IEA.

100, GO:0004281; F:metalloendopeptidase activity; IEA.

100, GO:0006586; ADAM_Cysteine.

100, GO:0006586; ADAM_Cysteine.

100, GO:0006586; ADAM_Cysteine.

100, GO:000686; ADAM_C
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PROSITE; PS50900; PLAC; 1.
PROSITE; PS50092; TSP1; 6.
PROSITE; PS00142; ZINC_PROTEASE; UNKNOWN_1.
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SEQUENCE FROM N.A.
STRIME-Bristol N2;
MEDLINE-99069613; PubMed-9851916;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A. STRAIN=C57BL/6; TISSUE=Brain;
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Matches 10; Conservative
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SMART; SM00209; TSP1; 7.
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SEQUENCE FROM N.A.
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Q8MYA8
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Pubmed=15192113; DOI=10.1074/jbc.M402380200;
Somerville R.P.T., Longpre J.M., Apel E.D., Lewis R.M., Wang L.W.,
Sanes J.R., Leduc R., Apte S.S.;
"ADAMTS7B, the full-length product of the ADAMTS7 gene, is a
chondroithin sulfate proteoglycan containing a mucin domain.";
J. Biol. Chem. 279:35159-3517.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Name=Rdamts7;
Mus musculus (Mouse).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ;
0
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Pred. No. 0.47;
1; Mismatches 1; Indels
"Genome sequence of the nematode C.elegans: A platform for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1461 AA; 162615 MW; 3CFDC1C07C1F493A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                         Wormerson (2014.1) CE31872.

ROGO GO:0004221; F:metalloendopeptidase activity; IEA.

ROGO GO:0004222; F:metalloendopeptidase activity; IEA.

GO: GO:000508; F:metalloendopeptidase activity; IEA.

InterPro; IPR001590; Peptidase_M12B.

InterPro; IPR001525; Pept M_Zn_BS.

InterPro; IPR001525; Pept M_Zn_BS.

InterPro; IPR001584; TSP1.

R PFam; PF001421; REProlyain; 1.

R PFam; PF001421; REPIALPEAT.

R RWART; SM00209; TSP1; 12.

R PROSITE; PS500215; ADAM_MEPRO; 1.

R PROSITE; PS500215; ADAM_MEPRO; 1.

R PROSITE; PS500215; ZINC_PROTEASE; UNKNOWN_1.
                                                                                                                                                                 25-OCT-2004 (TrEMBLrel. 28, Created)
25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT; 1641 AA.
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Interpro; IPR010294; ADAM spacer1.
Interpro; IPR0101590; Peptidase M12B.
Interpro; IPR0002870; Peptidase M12B.
Interpro; IPR0060287; Peptidase M12B.N.
Interpro; IPR006028; Pept M.Zn.BS.
Interpro; IPR00884; TSPI.
                                                                                                                                                                                                                                       EMBL, Z50004, CAA90293.2; -... EMBL, Z50006, CAA90293.2; JOINED. EMBL, Z50004; CAA90302.2; JOINED. EMBL, Z50006, CAA90302.2; -.. HSSP, P07996; LLSL.
                                                                                                                                                                                                                                                                                                                                                                                                WormBase; WBGene00000082; adt-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pfam; PF05986; ADAM_spacer1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        87.0%;
83.3%;
                                   investigating biology.";
Science 282:2012-2018(1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1088 WSDWSSCSKSCG 1099
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Matches 10; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 protein.
                                                                                                               SEQUENCE FROM N.A. STRAIN-Bristol N2;
                                                                                                                                                                                                                                                                                                                                                                             MEROPS; M12.302; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hypothetical
SEQUENCE 14
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125 AA.

Pfam; PF01562; Pep_M12B_propep; 1.

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Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                    "Genome sequence of the nematode C. elegans: a platform for investigating biology. The C. elegans Sequencing Consortium."; Science 282:2012-2018(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                "The sequence of C. elegans cosmid F08C6."; Submitted (JUN-1995) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Waterston R.;
Submitted (APR-2003) to the EMBL/GenBank/DDBJ databases.
                                                                                    01-0CT-2003 (TrEMBLrel. 25, Created)
01-0CT-2003 (TrEMBLrel. 25, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
Adants family protein 2, isoform b.
Name=adt-2; ORFNames=F08C6.1;
                                                                                                                                                                                                                                                                               STRAIN=Bristol N2;
MEDLINE=99069613; PubMed=9851916;
                                                       PRELIMINARY;
                                                                                                                                                                     Caenorhabditis elegans.
                                                                                                                                                                                                                                                                                                                        WormBase Consortium;
                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE PROM N.A. STRAIN-Bristol N2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A. STRAIN=Bristol N2;
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                                                                                                                                                                                                                                 NCBI_TaxID=6239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bentley D.;
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                                                     072292
                    RESULT 13
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Sukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Cetartiodactyla, Ruminantia, Pecora, Bovidae,
Bovines, Bos.
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                                                                                                                                                                                         87.0%; Score 67; DB 2; Length 1641;
83.3%; Pred. No. 0.52;
ive 0; Mismatches 2; Indels
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83.3%; Pred. No. 0.72;
ive 0; Mismatches 2; Indels
           PÉAM; PRO1421; REPTOLYSIN; 1.
PÉAM; PRO1421; REPTOLYSIN; 1.
PÉAM; PRO1009; TSP 1; 6.
PRINTS; PR01005; TSP 1; 6.
SMART; SM00009; ACR; 1.
SMART; SM00209; ACR; 1.
PROSITE; PS50021; ADAM MEPRO; 1.
PROSITE; PS50092; TSP 1; 6.
PROSITE; PS0092; ATNOT PROTEASE; UNKNOWN 1.
SEQUENCE 1641 AA; 180743 MM; BA3B1E7B492D6165 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gobron S., Creveaux I., Didier R., Meiniel R.;
Submitred (MAR-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AJ133488; CAB46239.1; -.
HSSP; P07996; 1LSL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1637 AA; 173346 MW; 4C5BAB1DD346C925 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                           Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                          PRT; 1637 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GO; GO: 0005576; C: extracellular; IEA.
GO; GO: 0005576; C: extracellular; IEA.
GO; GO: 0005179; F: hormone activity; IEA.
InterPro; IPR006207; Cys knot C.
InterPro; IPR001545; Gly_hormoneB.
InterPro; IPR001545; Gly_hormoneB.
InterPro; IPR00164; TSPI.
InterPro; IPR001694; TSPI.
InterPro; IPR001007; VWP_C.
Pfam; PP0101826; TIL1; 3.
Pfam; PP00093; VWC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PROSITE; PS01225; CTCK 2; 1.
PROSITE; PS00261; GLYCO_HORMONE_BETA_1; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                             Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PROSITE; PS00261; GLYCO HORMONE_BET#
PROSITE; PS50092; TSP1; 11.
PROSITE; PS01208; VWFC_1; UNKNOWN_1
PROSITE; PS50184; VWFC_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                     01-NOV-1999 (TrEMBLrel, 12, 01-NOV-1999 (TrEMBLrel, 12, 01-MAR-2004 (TrEMBLrel, 26, SCO-spondin (Fragment).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRINTS; PRO1705; TSPIREPEAT SWART; SMO0041; CT; 1. SWART; SMO1068; CHB; 1. SWART; SMO1209; TSP1; 11. SWART; SMO1214; VWC; 2.
                                                                                                                                                                                                                                                                                                  529 WSAWSDCSRSCG 540
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Best Local Similarity 83.3
Matches 10; Conservative
                                                                                                                                                                                                                                                                 1 WSGWSSCSRSCG 12
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Matches 10; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Name=sco-spondin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=9913;
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SEQUENCE
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Q9XSV8
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                                                                                                                                                                                                                                                                                                          Score 65; DB 2; Length 125;
Pred. No. 0.1;
0; Mismatches 2; Indels
Wilson R.;
Submitted (MAY-2003) to the EMBL/GenBank/DDBJ databases.
                                                                                                              to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cryptosporidium parvum.
Bukaryota, Alveolata, Apicomplexa, Coccidia, Bimeriida,
Cryptosporidiidae, Cryptosporidium.
                                                                                                                                                                                                           Pfam; PF00090; TSP 1; 2.
SMART; SM0209; TSP1; 2.
PROSITE; PS50092; TSP1; 2.
SEQUENCE 125 AA; 13940 MW; CS72F021DE87A468 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-NOV-1998 (TrEMBLrel. 08, Last sequence update) 01-MAR-2004 (TrEMBLrel. 26, Last annotation update) Thrombospondin-related adhesive protein (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             238 AA.
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                                                                                                                              EMBL; U29378; AAP40540.1; -.
WormBase; WBGene00000083; adt-2.
                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 83.3%;
Matches 10; Conservative
                                                                                                                                                                       WormPep; F08C6.1b; CB33991.
InterPro; IPR000884; TSP1.
                                                                                                                                                                                                                                                                                                                                                                                        1 WSGWSSCSRSCG 12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
                                                                                            WormBase Consortium;
Submitted (SEP-2004)
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648 WSAWSPCSRSCG 659

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Bos taurus (Bovine).
Bus taurus (Bovine).
Busaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovinae; Bos.
10 NCB TaxID=9913;
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2 TISSUB-Subcommissural organ; TISSUB-Subcommissural organ; Caeveaux I., Monnerie H., Elbitar F.; Gobron S., Creveaux I., Monnerie H., Elbitar F.; Submitted (OCT-1998) to the EMBL/GenBank/DDBJ databases. R EMBL; AJ132106; CAB53759.1; -I. RSP; Q90248; IHX2. R InterPro; IPR002919; Cysrich TIL. R InterPro; IPR000941; PMP SGCI. R InterPro; IPR00084; TSPI. R InterPro; IPR000885; TSPI. R InterPro; IPR006855; VWC_out.
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84.4%; Score 65; DB 2; Length 238;
Best Local Similarity 75.0%; Pred. No. 0.18;
Matches 9; Conservative 2; Mismatches 1; Indels
                                                                                                                     Spans F., Puttignani L., Crisanti A.;
Spans F., Puttignani L., Crisanti A.;
Submitted (JUN-1998) to the EMBL/GenBank/DDBJ databases.
EMBL; AF073838; AAC26812.1; -.
HSSP, P07996; ILSL.
InterPro; IPR002086; Aldehyd_dehydrog.
InterPro; IPR002086; TSP1.
Ffam; PR00009; TSP1; 3.
PROSITE; PS000070; ALDEHYDE_DEHYDR_CYS; UNKNOWN_I.
PROSITE; PS50092; TSP1; 3.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         238 AA; 26307 MW; 28242DE88F62C5A2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
11-MAX-2004 (TrEMBLrel. 26, Last annotation update)
SCO-spondin (Fragment).
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Pfam; PF00090; TSP 1; 6.
PRINTG; PR01705; TSP1REPEAT.
SMART; SM00209; TSP1; 6.
PROSITE; PS50092; TSP1; 6.
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Best Local Similarity 83.3
Matches 10; Conservative
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NCBI_TaxID=5807;
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Search completed: April 1, 2005, 13:59:23

341 WGPWSSCSRSCG 352

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1 WSGWSSCSRSCG 12

Job time : 77.6522 secs

GenCore version 5.1.6 Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

April 1, 2005, 13:43:07; Search time 16.6957 Seconds (without alignments) 69.156 Million cell updates/sec Run on:

US-09-462-909D-8 Title: Perfect score: Sequence:

1 WSGWSSCSRSCG 12

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283416 seqs, 96216763 residues Searched:

283416 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

PIR 79:*
I: Dirr:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	andiodenesis inhib	hypothetical prote	Δ.	hypothetical prote	hypothetical prote	-	hypothetical prote	•–	F-spondin - rat	hypothetical prote	F-spondin precurso	thrombospondin 1 p	~	thrombospondin 2 p	in pr	hypothetical prote		hypothetical prote		cartilage intermed	brain-specific and	•	unc-5 protein, lon	hypothetical prote	brain-specific and	hypothetical prote		_	_
SUMMARIES	ID	T18856	T15976	T18397	T16557	T16892	T00027	T22545	TSHUP1	A38152	T29247	A47723	A40558	TSHUP2	A42587	A39804	T19477	A48569	T25061	T34212	T09484	T00026	T32541	B44294	T00326	T00028	T21371	T47158	T16761	m
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	Query Match Length	1444	957	2098	551	860	1572	1059	1170	807	654	803	1170	1172	1172	1178	651	724	788	802	1184	1584	919	947	984	1522	2165	550	610	837
de	Query	87.0	84.4	83.1	79.2	79.2	79.2	77.9	77.9	9.9/	75.3	75.3	75.3	75.3	75.3	75.3	74.0	74.0	72.7	72.7	72.7	72.7	71.4	71.4	71.4	71.4	71.4	70.1	70.1	70.1
	Score	67	65	64	61	61	61	9	9	59	28	28	28	28	28	58	57	57	26	99	26	26	22	55	52	52	52	54	54	54
	Result No.	-	7	e	4	ហ	9	7	80	0	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	29

1071 WSDWSSCSKSCG 1082

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RESULT 2 T15976

1 WSGWSSCSRSCG 12

hypothetical protein F08C6.1 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Accession: T1S976
R;Bentley, D.
Submitted to the EMBL Data Library, June 1995
A;Description: The sequence of C. elegans cosmid F08C6.
A;Reference number: Z18440
A;Reference number: Z18440
A;Reference number: L1S976
A;Residues: 1-957 <-- REN>

gene ADAMTS-1 prot semaphorin F precu	coccidiosis-relate immunodominant mic	hypothetical prote hypothetical prote	procollagen N-endo TRAP-C2 protein -	hypothetical prote hypothetical prote	complement C6 prec	NOV protein - chic	gene CYR61 protein	hypothetical prote	thrombospondin-rel
T00017 JC5928	A45517 A45638	T19366 T00260	T18517 S49108	T14764 T33922	A34372 T21064	820078	A35669	T32570	804531
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951 1074	206 712	736 951	1205	898 1360	934	351	379	324	559
70.1	68.8 68.8	68.8 68.8	68.2	67.5	66.2	64.9	64.9	63.6	63.6
5 4	23 23	53 53	52.5	25 27	51	20	20	49	49
О н	<u>0 m</u>	4.2	36	8 8	9 :	42	13	4.	5

ALIGNMENTS

-	RESULT 1 T18856 angiogenesis inhibitor homolog - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Date: 15-Oct-1999 #text_change 09-Jul-2004 C;Accession: T18856; T24653
	R;McMurray, A. R;McMurray, A. R;Reference number: Z19031 A;Recession: T18856
	A; Scaus: printmary; translated iron GB/BMBL/DDBU A; Molecule type: DNA A; Residues: 1-1444 <wil> A; Cross-references: UNIPROT:QBMYA8; EMBL:Z50004; PIDN:CAA90293.1; GSPDB:GN00028; CESP:CO: A; Experimental source: clone C02B4 R; McMurray, A.</wil>
	submitted to the EMBL Data Library, July 1995 A;Reference number: Z19917 A;Accession: T24653 A;Status: preliminary; translated from GB/EMBL/DDBJ A;Molecule type: DNA A;Residues: 1-1444 <wiz></wiz>
	A;Cross-references: EMBL:Z50006; PIDN:CAA90302.1; GSPDB:GN00028; CESP:C02B4.1 A;Experimental source: clone T07C5 C;Genetics: A;Gene: CESP:C02B4.1 A;Map position: X
	A;Introns: 25/3; 70/3; 96/3; 139/3; 187/1; 234/2; 282/3; 376/2; 422/2; 478/3; 569/3; 566, Query Match Query Match Best Local Similarity 83.3%; Pred. No. 0.12; Matches 10; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

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Gaps

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A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: mRNAA
A;Rossule 1-1572 <SH1>
A;Cross-references: UNIPROT:060241; EMBL:AB005298; NID:g3021698; PIDN:BAA25362.1; PID:g30
A;Experimental source: brain
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A;Residues: 1-1059 <WLL>
A;Cross-references: UNIPROT:P90884; EMBL:Z81086; PIDN:CAB03121.1; GSPDB:GN00019; CESP:F5
A;Cross-imental source: clone F53B6
                                                                                                                                                                                                                                                                                                                       A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Actaus: preliminary; translated from GB/EMBL/DDBJ
A;Actaus: 1-860 <BEN>
A;Cross-references: UNIPROT:022580; EMBL:U42846; NID:g1125809; PID:g1125810; PIDN:AAA8360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A,Introns: 56/3; 96/1; 171/3; 199/3; 245/2; 293/2; 335/3; 395/3; 426/3; 484/2; 505/3; 582
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C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T22545
C;Species: Caenorhabditis elegans
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
C;Accession: T16892
R;Bentley, D.
Submitted to the EMBL Data Library, December 1995
A,Description: The sequence of C. elegans cosmid T19D2.
A,Reference number: Z18599
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          brain-specific angiogenesis inhibitor 2 - human
N,Alternate names: BAI2 protein
C,Species: Homo sapiens (man)
C,Date: 22-Jan-1999 #sequence_revision 22-Jan-1999 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rishiratsuchi, T.; Nishimori, H.; Ichise, H.; Nakamura, Y.; Tokino, T. Cytogenet. Cell Genet. 79, 103-108, 1997
A;Title: Cloning and characterization of BAI2 and BAI3, novel genes hom A;Reference number: Z14066; MUID:98194217; PMID:9533023
A;Accession: T00027
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Best Local Similarity 75.0%; Pred. No. 0.85;
Matches 9; Conservative 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       79.2%; Score 61; DB 2; Length 860; ilarity 75.0%; Pred. No. 0.55; Conservative 0; Mismatches 3; Indels
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A;Map position: 1p35-1p35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         358 WGSWSLCSRSCG 369
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Matches 9; Conserv
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C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Dates: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Ju1-2004
C;Accession: T1657
R;Nhan, M.
Submitted to the EMBL Data Library, October 1995
A;Description: The sequence of C. elegans cosmid K04E7.
A;Reference number: 218635
A;Accession: T1657
A;Reference number: 218636
A;Reference type: DNA
A;Residues: 1-531 <NHA>
A;Crossion: 10-51 <NHA
A;Crossion: 10-51 <NHA>
A;Crossion: 10-51 <NHA
A;C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               protein CTRP - malaria parasite (Plasmodium falciparum)
C;Species: Plasmodium falciparum
C;Species: Dlasmodium falciparum
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
B;Tocttein, F: Triglia, T.; Cowman, A.F.
Mol. Blochem. Parasitol. 74, 129-142, 1995
Mol. Blochem. Parasitol. 74, 129-142, 1995
A;Reference number: Z18926; MulD:96360471; PMD:8719155
A;Recession: T18397
A;Recession: T18397
A;Recession: T18397
A;Redidues: Jr-2098 <TRO>
A;Residues: 1-2098 <TRO>
A;Residues: 1-2098 <TRO>
A;Cross-references: UNIPROT:025757; EMBL:U34363; NID:g1098897; PID:g1098898; PIDN:AAC468
                                               A;Cross-references: UNIPROT:Q19204; EMBL:U29378; NID:g868184; PID:g868185; PIDN:AAA68721
A;Experimental source: strain Bristol N2
C;Genetics:
A;Gene: CESP:F08C6.1
A;Gene: C28P:F08C6.1
A;Introns: 23/1; 135/3; 220/3; 285/3; 325/2; 376/3; 461/2; 498/3; 532/3; 627/2; 714/1; 7
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Pred. No. 0.42;
2; Mismatches 1; Indels
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Pred. No. 0.39;
2; Mismatches 2; Indels
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84.4%; Score 65; DB 2; Length 957;
Best Local Similarity 83.3%; Pred. No. 0.17;
Matches 10; Conservative 0; Mismatches 2; Indels
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Best Local Similarity 66.7%;
Matches 8; Conservative
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Best Local Similarity 75.0%;
Matches 9; Conservative
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Gaps

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8

Score 60; DB 2; Pred. No. 0.87; 3; Mismatches

77.98; 66.78;

Query Match 77.9 Best Local Similarity 66.7 Matches 8; Conservative

ò a thrombospondin 1 precursor - human

A; Accession: A26155

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Superfamily: thrombospondin 1; EGF homology; thrombospondin type 1 repeat homology; vor CiRepartamily: thrombospondin 1; EGF homology; thrombospondin type 1 repeat homology; vor CiRepartamily: thrombospondin 1; EGF homology; thrombospondin type 1 repeat homology; vor CiRepartamily: beta-hydroxyasparagine; calclum binding; cell adhesion; glycoprotein; trimer Fil-18/Domain: signal sequence #status predicted <510.
Fil-9-1170/Product: thrombospondin 1 #status predicted <MAT>
Fil-317-375/Domain: thrombospondin type 1 repeat homology <THR2>
Fil-344-490/Domain: thrombospondin type 1 repeat homology <THR2>
Fil-551-586/Domain: thrombospondin type 1 repeat homology <THR3>
Fil-551-586/Domain: EGF homology <EGF2>
Fil-551-588/Domain: EGF homology <EGF2>
Fil-22/Disulfide bonds: #status predicted
Fil-22/Disulfide bonds: #status predicted
Fil-23/Disulfide bonds: #status predicted
Fil-20/Cirepartamin EGF homology <EGF2>
Fil-20/Disulfide bonds: #status predicted
Fil-20/Disulfide bonds: #status predicted
Fil-20/Disulfide bonds: #status predicted
Fil-20/Disulfide ste: erythro-beta-hydroxyasparagine (Asn) #status predicted
Fil-20/Disulfide ste: erythro-beta-hydroxyasparagine (Asn) #status absent
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C;Accession: A38152
R;Klar, A.; Baldassare, M.; Jessell, T.M.
C211 69, 95-110, 1992
A;Title: F-spondin: a gene expressed at high levels in the floor plate encodes a secretec A;Reference number: A38152; MUID:92208952; PMID:1555244
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A;Molecule type: mRNA
A;Residues: 1-807 <KLA>
A;Ecoss-references: UNIPROT:P35446; GB:M88469; NID:g204176; PIDN:AAA41174.1; PID:g204177
A;Experimental source: embryo floor plate
A;Note: sequence extracted from NCBI backbone (NCBIN:90877, NCBIP:90878)
C;Superfamily: F-spondin; thrombospondin type 1 repeat homology
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C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accssion: T29247
R;Minx, P.; Hawkins, J.
submitted to the EMBL Data Library, November 1995
A;Description: The sequence of C. elegans cosmid F09F9.
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Pred. No. 0.93;
1; Mismatches 2; Indels
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            Note: the list of introns may be incomplete; Complex: homotrimer, disulfide linked
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C;Species: Rattus norvegicus (Norway rat)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        77.9%;
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66.7%;
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Matches 9; Conserv
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Matches 8; Conserv
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A; Residues: 1-83, 47, 85-522, 47, 524-1170 cHEN>
A; Residues: 1-83, 47, 85-522, 47, 524-1170 cHEN>
A; Residues: 1-83, 47, 85-522, 47, 1012937464; PIDN:CAA32889.1; PID:g37465
A; Note: parts of this sequence, including the amino end of the mature protein, were dete
R; Kobayashi, S.; Eden-McCutchan, F.; Framson, P.; Bornstein, P.
Biochemistry 25, 8418-8425, 1986
A; Title: Partial amino acid sequence of human thrombospondin as determined by analysis c
A; Reference number: A25812; MUID:87157592; PMID:3030396
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A; Residues: 1-83,'A',85-374,'RC' <DIX>
A; Cross-references: GB:M14126; NID:G340005; PIDN:AAAG1237.1; PID:G553801
A; Note: parts of this sequence, including the amino end of the mature protein, were dete
R; Sun, X.; Skorstengaard, K.; Mosher, D.F.
J. Cell Biol. 118, 693-701, 1992
A; Title: Disulfides modulate RGD-inhibitable cell adhesive activity of thrombospondin.
A; Reference number: A42927; MUID:92348511; PMID:1379247
A;Map position: 1
A;Introns: 38/3; 92/3; 131/3; 169/1; 236/2; 282/3; 349/2; 376/2; 420/1; 576/3; 759/3; 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Molecule type: DNA
Residues: 1-166 cLAH>
Residues: 1-166 cLAH>
Hennessy, S.W.; Frazier, B.A.; Kim, D.D.; Deckwerth, T.L.; Baumgartel, D.M.; Rotwein,
Cell Biol. 108, 729-736, 1989
Tiftle: Complete thrombospondin mRNA sequence includes potential regulatory sites in th
Reference number: A30140; WUID:89139590; PMID:2918029
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A Molecule type: mRNA

A Residues: 1-110 <LAM

A; Residues: 1-110 <LAM

A; Cross-references: UNIPROT.P07996; GB:X04665; NID:g37137; PIDN:CAA28370.1; PID:g37138

A; Note: parts of this sequence, including the amino end of the mature protein, were dete

A; Note: parts of this sequence, including the amino end of the mature protein, were dete

A; Laherty, C.D.; Gierman, T.M.; Dixit, V.M.

J. Blool. Chem. 264, 11222-11227, 1989

A; Title: Characterization of the promoter region of the human thrombospondin gene. DNA &

A; Reference number: A34274; MUID:89291870; PMID:2544587
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C;Species: Homo sapiens (man)
C;Date: 23-Aug-1997 #sequence_revision 03-Aug-1995 #text_change 09-Jul-2004
C;Date: 23-Aug-1997 #sequence_revision 03-Aug-1995 #text_change 09-Jul-2004
C;Accession: A.34174; A30140; A25812; A05172; A42927
R;Lawler, J.; Hynes, R.O.
J. Cell Biol. 103, 1635-1648, 1986
A;Title: The structure of human thrombospondin, an adhesive glycoprotein with multiple A;Reference number: A26155; MUID:87057617; PMID:2430973
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A; Residues: 1-83, A', 85-397 < KOB>

A; Residues: 1-83, A', 85-397 < KOB>

A; Cross-references: GB:M25631; NID:g538353; PIDN:AAA36741.1; PID:g538354

B; Dixit, V.M.; Hennessy, S.W.; Grant, G.A.; Rotwein, P.; Frazier, W.A.

Proc. Natl. Acad. Sci. U.S.A. 83, 5449-5453, 1986

A; Reference number: A05172; MUID:86287276; PMID:3461443
                                                                                                                                                                                                              ö
                                                                                                                           Length 1059
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A;Molecule type: protein A;Residues: 987-1003 <SUN> A;Note: Cys-992 is shown to have a free sulfhydryl

Accession: A42927

A,Gene: GDB:THBS1; TSP1; TSP A,Cross-references: GDB:120438; OMIM:188060 A,Map position: 15q15-15q15

A; Introns: 23/1

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A)Description: participates in cell migration and adhesion, and in platelet aggregation C,Superfamily: thrombospondin 1; EGF homology; thrombospondin type 1 repeat homology; vo C;Superfamily: thrombospondin 1; EGF homology; thrombospondin greal adhesion; glycoprotein; rimer E;1-18/Domain: signal sequence #status predicted <SIG>F;1-18/Domain: signal sequence #status predicted <SIG>F;19-1172/Product: thrombospondin 2 #status predicted <MAT>F;19-177/Domain: von Willebrand factor type C repeat homology <VWC>
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Rilabell, T.L.; Byers, P.H.
Apritie: Sequence and characterization of the complete human thrombospondin 2 cDNA: poter
A,Ritle: Sequence and characterization of the Complete human thrombospondin 2 cDNA: poter
A,Reference number: A47379; MUID:94010892; PMID:8406456
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Molecule type: protein
C; Complex: homoropondin 1; EGF homology; thrombospondin 1 #status predicted <MIG-
F; 11-18 Domain: signal sequence #status predicted <MMT-
F; 11-18 Domain: thrombospondin 1 #status predicted <MMT-
F; 11-18 Domain: thrombospondin type 1 repeat homology <THR1-
F; 11-18 Domain: thrombospondin type 1 repeat homology <THR2-
F; 11-18 Domain: thrombospondin type 1 repeat homology <THR2-
F; 11-18 Domain: thrombospondin type 1 repeat homology <THR2-
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F; 11-18 Domain: thrombospondin type 1 repeat homology <THR2-
F; 11-18 Domain: throm
J. Biol. Chem. 267, 3274-3281, 1992
J. Biol. Chem. 267, 3274-3281, 1992
A. Fitle: Characterization of mouse thrombospondin 2 sequence and expression during cell & A. Reference number: A42867; MUID:92147683; PMID:1371115
A. Accession: B42587
A. Accession: B42587
A. Accession: B42587
A. Accession: B42587
                                                                                                                                                                                           A; Molecule type: mRNA
A; Molecule type: mRNA
A; Molecule type: mRNA
A; Molecule type: mRNA
A; Cross-references: GB: M87276
A; Note: sequence extracted from NCBI backbone (NCBIP: 81501)
A; Note: sequence extracted from NCBI backbone (NCBIP: 81501)
A; Note: sequence extracted from NCBI backbone (NCBIP: 81501)
A; Note: sequence extracted from NCBI backbone (NCBIP: 81501)
A; Title: Expression and initial characterization of recombinant mouse thrombospondin 1 & A; Reference number: 868787; MUID: 96234006; PMID: 8654563
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C.Date: 19-May-1995 #sequence_revision 03-Aug-1995 #text_change 09-Jul-2004
C.Accession: A47379; A42173
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A;Residues: 560-1172 <LA2>
A;Cross-references: GBHN81339
A;Experimental source: fibroblast
A;Nore: sequence extracted from NCBI backbone (NCBIN:95091, NCBIP:95096)
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                                                                                                                                                          A, Status: preliminary, not compared with conceptual translation
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A;Cross-references: GDB:128789; OMIM:188061
A;Map position: 6427-6427
C;Complex: homotrimer, disulfide linked
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441 WSPWSSCSVTCG 452
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Best Local Similarity
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A, Status preliminary
A, Status preliminary
A, Molecule type: DNA
A, Residues: 1-1170 < LDAN
A, STATE (B: M62469; GB: M62466; GB: M62469; GB: M62469; GB: M62470; NID: GS: M82464; GB: M62461; GB: M62469; GB: M62469; GB: M62469; GB: M62470; NID: GS: M925116
A, M925116: Characterization of the mouse thrombospondin gene and evaluation of the role of A, Reference number: A37905; MUID: 90375546; PMID: 2398070
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P. Spondin precursor - African clawed frog
F. spondin precursor - African clawed frog)
C. Species: Xenopus laevis (African clawed frog)
C. Species: Xenopus laevis (African clawed frog)
C. Accession: A47723
R. Species: A11224
R. Species: A2-Jun-1994 #sequence_revision 27-Jun-1994 #text_change 09-Jul-2004
C. Accession: A1723
R. Species: A1723
R. Species: A2723
R. S
A;Reference number: Z20594
A;Accession: T29247
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Notecule type: DNA
A;Residues: 1-654 «MIN>
A;Residues: 1-654 «MIN>
A;Cross-references: UNIPROT:Q19284; EMBL:U40958; PIDN:AAA81764.1; CESP:F09F9.4
C;Genetics: A;Gene: CESP:F09F9.4
A;Cntrons: 89/3; 138/3; 192/3; 260/1; 312/1; 400/2; 445/3; 496/1; 523/1; 558/2; 596/2
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C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Daceses: Mus musculus (species)
C;Dacesesion: A40558; A37905; B42587; S68787
R;Lawler, J.; Duquette, M.; Perro, P.; Copeland, N.G.; Gilbert, D.J.; Jenkins, N.A. Genomics 11, 587-600, 1991
A;Title: Characterization of the murine thrombospondin gene.
A;Reference number: A40558; MUID:92128941; PMID:1774063
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
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Pred. No. 1.3;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 58; DB 2;
Pred. No. 1.1;
2; Mismatches
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Best Local Similarity 66.7%;
Matches 8; Conservative
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322 WSEWSACSETCG 333
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A;Molecule type: DNA
A;Residues: 1-490 <BOR>
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Matches 8; Conserv
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A; Status: preliminar
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RESULT 12

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Gaps

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A;Molecule type: mRNA
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Cross-references uNIPROT:P35440; GB:M60853; NID:g212763; PIDN:AAA51437.1; PID:g212764
A;Cross-references uNIPROT:P3540; GB:M60859; thrombospondin type 1 repeat homology vor
C;Superfamily: thrombospondin type 1 repeat homology <VWC>
F;325-383/Domain: thrombospondin type 1 repeat homology <THRI>
F;424-498/Domain: thrombospondin type 1 repeat homology <THRI>
F;459-555/Domain: thrombospondin type 1 repeat homology <THRI>
F;658-697/Domain: EGF homology <EGF>
                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 58; DB 1; Length 1178;
Pred. No. 1.8;
1; Mismatches 2; Indels
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Best Local Similarity 75.0
Matches 9; Conservative
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                                                    A;Status: preliminary
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F;380-431/Domain: thrombospondin type 1 repeat homology <THR1>
F;436-492/Domain: thrombospondin type 1 repeat homology <THR2>
F;436-492/Domain: thrombospondin type 1 repeat homology <THR2>
F;493-4949/Domain: thrombospondin type 1 repeat homology <THR3>
F;552-691/Domain: EGF homology <EGF>
F;526-930(Region: Cell attachment (R-G-D) motif
F;151,316,330,457;584,710,1069/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;167-226/Disulfide bonds: interchain #status predicted
F;266,270/Disulfide bonds: interchain #status predicted
F;612/Modified site: erythro-beta-hydroxyasparagine (Asn) #status predicted
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C;Superfamily: thrombospondin 1; EGF homology; thrombospondin type 1 repeat homology; vc
C;Reywords: calcium binding; glycoprotein
E;319-377/Domain: von Willebrand factor type C repeat homology <VWC>
F;380-431/Domain: thrombospondin type 1 repeat homology <THR1>
F;436-492/Domain: thrombospondin type 1 repeat homology <THR2>
F;431-549/Domain: thrombospondin type 1 repeat homology <THR3>
F;553-588/Domain: EGF homology <EGF>
F;652-691/Domain: EGF homology <EGF>
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R;Lahorty, C.D.; O'Rourke, K.; Wolf, F.W.; Katz, R.; Seldin, M.F.; Dixit, V.M.
B;Ol. Chem. 257, 3274-3281, 1992
A;Title: Characterization of mouse thrombospondin 2 sequence and expression during cell A;Reference number: A42587; WUID:92147683; PMID:1371115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Molecule type: nucleic acid
A; Residues: 1-173 cLAH;
A; Cross-references: UNIPROT (203350; GB:L07803; GB:M87275; NID:g340421; PIDN:AAA53064.1;
A; Cross-references: UNIPROT from NCBI backbone (NCBIP:81502)
B; Bornstein, P.; O'Rourke, K.; Wikstrom, K.; Wolf, F.W.; Katz, R.; Li, P.; Dixit, V.M.
Biol. Chem. 266, 12821-12824, 1991
A; Title: A second, expressed thrombospondin gene (Thbs2) exists in the mouse genome.
A; Reference number: A39851; MUID:91302287; PMID:1712771
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C;Species: Mus musculus (house mouse)
C;Date: 04-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    thrombospondin precursor - chicken
C;Species: Gallus gallus (chicken)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C;Accession: A39804
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                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 75.3%; Score 58; DB 1; Length 1172; Best Local Similarity 75.0%; Pred. No. 1.7; Matches 9; Conservative 1; Mismatches 2; Indels
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A, Title: Cloning and sequencing of chicken thrombospondin. A, Reference number: A39804; MUID:91217026; PMID:2022631
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              443 WSPWSSCSVTCG 454
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Best Local Similarity 75.v.
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us-09-462-909d-8) rapb
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GenCore version 5.1.6 Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

April 1, 2005, 13:59:39 ; Search time 61.8261 Seconds (without alignments) 64.360 Million cell updates/sec Run on:

1 WSGWSSCSRSCG 12 US-09-462-909D-8 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5

Scoring table:

1413372 seqs, 331592847 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

- Published Applications AA:* Database :

/rodata/2/pubpaa/1809B PUBCOMB.pep:* /ptodata/2/pubpaa/1809G PUBCOMB.pep:* /ptodata/2/pubpaa/1809G NUB.pep:* /ptodata/2/pubpaa/1810A PUBCOMB.pep:* /ptodata/2/pubpaa/1810B PUBCOMB.pep:* 6/ptodata/2/pubpaa/PCT_NEW_PUB.ppp:*
6/ptodata/2/pubpaa/US06_NEW_PUB.ppp:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		Description	Sequence 5, Appli	Sequence 2, Appli	Sequence 7, Appli	Sequence 32, Appl	Sequence 1094, Ap	Sequence 23, Appl	Sequence 2, Appli	Sequence 5, Appli	Sequence 132, App	Sequence 89, Appl	Sequence 180, App	Sequence 196, App	Sequence 4, Appli
COLUMNICO		OI OI	US-10-213-509-5	US-10-085-198-2	US-09-918-171A-7	US-09-981-151A-32	US-10-408-765A-1094	US-10-312-352-23	US-10-386-414-2	US-09-788-043C-5	US-10-161-493-132	US-09-800-198-89	US-10-262-839-180	US-10-262-839-196	US-09-981-151A-4
		DB	14	15	6	10	16	15	15	σ	15	10	15	15	10
		Match Length DB	4123	4219	997	997	997	1255	1686	1690	353	415	571	577	791
	& Query	Match	88.3	88.3	84.4	84.4	84.4	84.4	84.4	84.4	83.1	81.8	81.8	81.8	81.8
		Score	89	68	65	65	65	65	65	65	64	63	63	63	63
	Result	No.	н	7	٣	4	2	9	7	α	6	10	11	12	13

Sequence 6, Appli Sequence 2, Appli Sequence 2, Appli Sequence 51, Appli Sequence 51, Appli Sequence 4, Appli Sequence 182, App Sequence 182, App Sequence 182, Appli Sequence 2, Appli Sequence 2, Appli Sequence 194, Appli Sequence 194, Appli Sequence 194, Appli Sequence 194, Appli Sequence 194, Appli Sequence 194, Appli Sequence 136, Appli Sequence 136, Appli Sequence 136, Appli Sequence 136, Appli Sequence 137, Appli Sequence 44, Appli	
US-09-981-151A-6 US-09-981-151A-8 US-09-981-151A-8 US-09-981-151A-8 US-10-296-616-2 US-10-296-616-2 US-10-296-616-2 US-10-296-616-2 US-10-262-839-184 US-10-262-839-184 US-10-262-839-186 US-10-262-839-186 US-10-262-839-186 US-10-262-839-186 US-10-262-839-186 US-10-262-839-136 US-10-262-839-138 US-10-262-839-138 US-10-262-839-138 US-10-161-493-138 US-10-161-493-138 US-10-161-493-138 US-10-161-493-138 US-10-161-493-139 US-10-161-493-139 US-10-161-493-139 US-10-181-186-132 US-10-181-186-132 US-10-181-186-132 US-10-181-186-132 US-10-181-186-132 US-10-181-186-133	
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ALIGNMENTS

RESULT 1
US-10-213-509-5
i Sequence 5, Application US/10213509
i Publication No. US20030054485A1
i GENERAL INFORMATION:
i APPLICANT: Weise, Joseph
i APPLICANT: Weise, Joseph
i TITLE OF INVENTION: UELLY BELLY GENES AND THEIR USES
I TILE REFERENCE: STAN-232
CURRENT APPLICATION NUMBER: US/10/213,509
CURRENT FILING DATE: 2002-08-06
i PRIOR APPLICATION NUMBER: 60/311,720
i PRIOR APPLICATION NUMBER: 60/311,720
i RILNG DATE: 2001-08-09
i NUMBER OF SEQ ID NOS: 5
i SOFTWARE: FRESEQ for Windows Version 4.0
i SEQ ID NO 5
i ENGTH: 4123 ; ORGANISM: H. sapiens US-10-213-509-5 TYPE: PRT

Query Match

88.3%; Score 68; DB 14; Length(4123;
Best Local Similarity 91.7%; Pred. No. 4.8;
Matches 11; Conservative 0; Mismatches 1; Indels (

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Gaps ö

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Sequence 2, Application US/10085198; Publication No. US20040009907A1; GENERAL INFORMATION: APPLICANT: Alsobrook et al. US-10-085-198-2

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CURRENT APPLICATION NUMBER: US/10/085,198

CURRENT FILING DATE: 2002-02-25

PRIOR FILING DATE: 2001-02-26

PRIOR FILING DATE: 2001-08-13

PRIOR FILING DATE: 2001-08-16

PRIOR FILING DATE: 2001-08-20

PRIOR FI
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APPLICANT: Apte, Sunce!
APPLICANT: Hurshainen, Tiina L.
APPLICANT: Hurshainen, Tiina L.
APPLICANT: Hirohata, Satoshi
TITLE OF INVENTION: Nucleic Acids Encoding Zinc Metalloproteases
FILE REFERENCE: 26473/04193
CURRENT APPLICATION NUMBER: US/09/918,171A
CURRENT APPLICATION NUMBER: 09/369,364
PRIOR APPLICATION NUMBER: 09/369,364
PRIOR FILING DATE: 1999-08-06
NUMBER OF SEQ ID NOS: 31
SOCTIVARE: Patentin Ver. 2.1
SEQ ID NO 7
LENGTH: 997
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Pred. No. 4.9;
0; Mismatches 1; Indels (
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TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 65; DB 9
Pred. No. 3.7;
0; Mismatches
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Patent No. US20020110894A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT CORGANISM: Homo sapiens ADAMIS-7
US-09-918-171A-7
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Best Local Similarity 83.3%;
Matches 10; Conservative
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Best Local Similarity 91.7%;
Matches 11; Conservative
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ORGANISM: Homo sapiens
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544 WSAWSICSRSCG 555

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APPLICANY: Guo, Xiaojia
APPLICANY: Guo, Xiaojia
APPLICANY: Taupier Jr. Raymond J
APPLICANY: Taupier Jr. Raymond J
APPLICANY: Burges, Catherine B
APPLICANY: Seriuse, Bryan D
APPLICANY: Gangolli, Esha A
APPLICANY: MUMBER: 60/241,040
PRIOR FILING DATE: 2000-10-17
PRIOR PLING DATE: 2000-10-17
PRIOR PLING DATE: 2000-10-17
PRIOR PLING DATE: 2000-10-17
PRIOR PLING DATE: 2000-10-27
PRIOR PLICATION NUMBER: 60/242,482
PRIOR FILING DATE: 2000-10-23
PRIOR FILING DATE: 2000-10-24
PRIOR PLING DATE: 2000-10-24
PRIOR FILING DATE: 2000-10-24
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Pred. No. 3.7;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-10-408-765A-1094
; Sequence 1094, Application US/10408765A
; Publication No. US20040101874A1
S-09-981-151A-32
Sequence 32, Application US/09981151A
Septication No. US20030212256A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ellerman, Karen
Shimkets, Richard A
Padigaru, Muralidhara
                                                                                                                          GENERAL INCORDATION:
GENERAL INCORDATION:
APPLICANT: Gerlach, Valerie
APPLICANT: MacDougall, John R
APPLICANT: Malyankar, Muriel M
APPLICANT: Smithson, Glennda
APPLICANT: Millet, Isabelle
APPLICANT: Peyman, John A
APPLICANT: Stone, David J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                84.4%;
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Best Local Similarity 83.3
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 WSGWSSCSRSCG 12
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Gaps
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APPLICANT: GOOK, WILLIAM James
APPLICANT: MACBEL, Kyle J.
APPLICANT: Garroll, Joseph M.
APPLICANT: Carroll, Joseph M.
APPLICANT: Chun, Miyoung
ITILE OF INVENTION: NOVEL 27875, 22025, 27420, 17906, 16319,
TITLE OF INVENTION: NOVEL 27875, 22025, 27420, 17906, 16319,
TITLE OF INVENTION: NOVEL 27875, 22025, 27420, 17906, 16319,
TITLE OF INVENTION: S5092 AND 10218 MOLECULES AND USES THEREFOR
FILE REPERENCE: MAPPLE 2003-03-11
PRIOR APPLICATION NUMBER: US/10/386,414
PRIOR FILING DATE: 2000-09-22
PRIOR PRILNG DATE: 1999-06-11
PRIOR FILING DATE: 2000-11-28
PRIOR FILING DATE: 2000-11-28
PRIOR FILING DATE: 2001-10-39
PRIOR FILING DATE: 2001-10-39
PRIOR FILING DATE: 2001-10-31
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                                                                                                                                                                                                                                                                                                        ; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. US20040053824A1 55022490CD1
US-10-312-352-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 65; DB 15;
Pred. No. 4.5;
0; Mismatches 2;
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0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Kapeller-Libermann, Rosana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 2, Application US/10386414
Publication No. US20040006016A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Robison, Keith B.
White, David
Williamson, Mark W.
Cook, William James
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     84.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 83.3%;
Matches 10; Conservative
PRIOR FILING DATE: 2000-11-16
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Best Local Similarity 83.3<sup>3</sup>
Matches 10, Conservative
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                            NUMBER OF SEQ ID NOS: 72
SOFTWARE: PERL Program
SEQ ID NO 23
LENGTH: 1255
TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 WSGWSSCSRSCG 12
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ORGANISM: Homo Sapien
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APPLICANT: INCYPE GENOMICS, INC.; TANG, Y. TOM
APPLICANT: HE, Ann; BATRA, Sajeev
APPLICANT: HE, Ann; BATRA, Sajeev
APPLICANT: LO, Terence P.; NGUYEN, Danniel B.
APPLICANT: LO, Terence P.; NGUYEN, Gregory A.
APPLICANT: ZINGLER, Kurt A.; GANDHI, Amena R.
APPLICANT: ZINGLER, Kurt A.; GANDHI, Amena R.
APPLICANT: GHAWIA, Narinder K.; ELLIOT, Vicki S.
APPLICANT: GHAWIA, Narinder K.; ELLIOT, Vicki S.
APPLICANT: ARVIZU, CHANDER S.; KHAN, Farizh A.
APPLICANT: POLICKY, Jennifer L.; AU-YOUNG, Janice K.
APPLICANT: LU, Yan; BOROWSKY, Mark L.
APPLICANT: LU, Dyung Aina M.; RAMKUWAR, Jayalaxmi
APPLICANT: YANG, Junming; GURUBAJAN, Rajagopal
APPLICANT: WARREN, Bridget A.; GIETZEN, Kavitha
APPLICANT: LU, Yuning, KALLICK, Deborah A.
APPLICANT: LU, SEREGEANE, ANGELO, A.
APPLICANT: LEE, SAILY
TITLE OF INVENTION: EXTRACELLULAR MATRIX AND CELL ADHESION MOLECULES
FILE REPERRUE: PP-0794 USN
FILE REPERR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                             APPLICANT: Gibson, Bradford W.
APPLICANT: Taylor, Steven W.
APPLICANT: Taylor, Steven W.
APPLICANT: Glenn, Gary W.
TITLE OF INVENTION: TAKGETS FOR THERAPEUTIC INTERVENTION
TITLE OF INVENTION: IDENTIFIED IN THE MITOCHONDRIAL PROTEOME
TITLE REFERENCE: 660088.465
CURRENT APPLICATION WHERE: US/10/408,765A
CURRENT FILING DATE: 2003-04-04
NUMBER OF SEQ ID NOS: 3077
SEQ ID NO 1094
LENGTH: 997
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83.3%; Pred. No. 3.7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2; Indels
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CURRENT FILING DATE: 2002-12-18
PRIOR APPLICATION NUMBER: ECT/USO1/21067
PRIOR FILING DATE: 2001-06-29
PRIOR PILING DATE: 2000-06-29
PRIOR PILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: US 60/215,454
PRIOR PILING DATE: 2000-07-18
PRIOR PILING DATE: 2000-07-18
PRIOR PILING DATE: 2000-10-12
PRIOR APPLICATION NUMBER: US 60/240,106
PRIOR APPLICATION NUMBER: US 60/244,021
PRIOR APPLICATION NUMBER: US 60/244,021
PRIOR APPLICATION NUMBER: US 60/244,021
PRIOR PAPLICATION NUMBER: US 60/246,871
PRIOR PILING DATE: 2000-10-27
PRIOR PAPLICATION NUMBER: US 60/246,871
PRIOR PILING DATE: 2000-11-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 23, Application US/10312352
Publication No. US20040053824A1
GENERAL INFORMATION:
                                Ghosh, Soumitra S. Fahy, Eoin D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 83.3
Matches 10; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; ORGANISM: Homo sapiens
US-10-408-765A-1094
                                                                                                                 Zhang, Bing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT
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CURRENT PILING DATE: 2002-3//A

CURRENT PILING DATE: 2001-06-03

PRIOR FILING DATE: 2001-06-04

PRIOR FILING DATE: 2001-06-04

PRIOR FILING DATE: 2001-06-04

PRIOR PILING DATE: 2001-16-06

PRIOR PELING DATE: 2001-16-06

PRIOR PELING DATE: 2001-06-06

PRIOR PELING DATE: 2001-06-06

PRIOR PELING DATE: 2001-06-06

PRIOR PELING DATE: 2001-06-06

PRIOR PILING DATE: 2001-06-06

PRIOR PILING DATE: 2001-06-07

PRIOR PILING DATE: 2001-06-07

PRIOR PILING DATE: 2001-06-07

PRIOR PILING DATE: 2001-06-07

PRIOR PILING DATE: 2001-06-11

PRIOR PILING DATE: 2001-06-12

PRIOR PILING DATE: 2001-06-13

PRIOR PILING DATE: 2001-06-13
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APPLICANT: Vernate, Cornie AM
APPLICANT: Fernandes, Elma
APPLICANT: Shimkets, Richard A
APPLICANT: Shimkets, Richard A
APPLICANT: Braman, John L
APPLICANT: Majunder, Kumud
APPLICANT: Majunder, Kumud
APPLICANT: Mases, Peter S
APPLICANT: Rastelli, Luca
APPLICANT: Rastelli, Luca
TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
FILE REFERENCE: 1596-6-67
CURRENT APPLICATION NUMBER: 60/186,596
FRICO FILING DATE: 2000-03-03
NUMBER OF SEQ ID NOS: 98
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 89
LENGTH: 415
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Pred, No. 3.3;
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Pred. No. 2.2;
1; Mismatches
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US-09-800-198-89
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Best Local Similarity 75.0%;
Matches 9; Conservative
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75.0%;
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Best Local Similarity 75.0
Matches 9; Conservative
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CORGANISM: Homo sapiens
US-10-161-493-132
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US-09-800-198-89
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TITLE OF INVENTION: No. US20040018555A1el Antibodies that Bind to Antigenic Polypepti
TITLE OF INVENTION: Acids Encoding the Antigens, and Methods of Use
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APPLICANT: ZULY, Fengrong
APPLICANT: ZULY, Fengrong
APPLICANT: Klonowski, Paul
TITLE OF INVENTION: No. US20020107361Alel Metalloproteases Having
TITLE OF INVENTION: Thrombospondin Domains and Nucleic Acid Compositions
TITLE OF INVENTION: Encoding the Same
FILE REFERENCE: ROCH-004
CURRENT APPLICATION NUMBER: US/09/788,043C
CURRENT PILING DATE: 2001-02-16
PRIOR PPLICATION NUMBER: 60/184,152
PRIOR FILING DATE: 2000-02-18
NUMBER OF SEQ ID NOS: 10
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 5
LENGTH: 1690
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83.3%; Pred. No. 5.6;
.ive 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 132, Application US/10161493
Publication No. US20040018555A1
GENERAL INFORMATION:
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Malyankar, Uriel M
Padigaru, Muralidhara
Ji, Weizhen
Smithson, Glennda
Edinger, Salomit R
Miller, Isabelle
                                                                                                                                                                             Sequence 5, Application US/09788043C patent No. US20020107361A1 GENERAL INFORMATION:
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Guo, Xiaojia Sasha
Miller, Charles E
Shenoy, Suresh G
Hjalt, Tord
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Gerlach, Valerie
Shinkets, Richard A
Gorman, Linda
Pena, Carol EA
Kekuda, Ramesh
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MacDougall, John R
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Spytek, Kimberly A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Anderson, David W
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        548 WSAWSICSRSCG 559
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                             Zhong, Mei
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Best Local Similarity
Matches 10; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Rastelli
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ORGANISM: human
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US-10-161-493-132
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US-09-788-043C-5
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124 WSNWSRCSKSCG 135

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320 WITWSSCSKSCG 331

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APPLICANT: Zhong, Mei
TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD
FILE REFERENCE: 21402-4624
CURRENT APPLICATION NUMBER: US/10/262,839
CURRENT PILING DATE: 2002-10-01
PRIOR PILING DATE: 2001-10-09
PRIOR PILING DATE: 2002-04-12
PRIOR PILING DATE: 2002-04-12
PRIOR PILING DATE: 2001-10-05
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NUMBER OF SEQ ID NOS: 367
SOFTWARE: CuraSeqList version 0.1
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Sequence 180, Application US/10262839
Publication No. US20040038877A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Miler, Charles,
Patturajan, Meera,
Reiger, Daniel,
Rothenberg, Mark,
Shimkets, Richard,
Smithson, Glemda,
Spytek, Kimberly,
Taupier, Raymond, jr.,
Vernet, Corine,
                                                                                                       LICANT: Alsobrook, John,
LICANT: Anderson, David W.,
LICANT: Boldog, Ferenc,
LICANT: Burgess, Catherine,
LICANT: Edinger, Shlomit,
LICANT: Elerman, Karen,
LICANT: Gerlach, Valerie,
LICANT: Gerlach, Valerie,
LICANT: Gorman, Linda,
LICANT: Gorman, Linda,
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Zerhusen, Brian,
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Kekuda, Ramesh,
Leach, Martin,
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Best Local Similarity 75.0
Matches 9; Conservative
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ORGANISM: Homo sapiens
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LENGTH: 571
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Pred. No. 4.3;
1; Mismatches
         Sequence 196, Application US/10262839 Publication No. US20040038877A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                            laupier, Raymond, jr.,
Vernet, Corine,
                                                        Boldog, Ferenc,
Burgess, Catherine,
Catterton, Elina,
Edinger, Shlomit,
Ellerman, Karen,
Gerlach, Valerie,
Gorman, Linda,
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Best Local Similarity 75.0%;
Matches 9; Conservative
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Shimkets, Richard,
Smithson, Glennda,
Spytek, Kimberly,
                                                                                                                                                                                    Patturajan, Meera
Reiger, Daniel,
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Voss, Edward,
Zerhusen, Brian,
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Leach, Martin,
                                                                                                                          uo, Xiaojia,
i, Weizhen,
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JS-10-262-839-196
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Gaps

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125 WSNWSRCSKSCG 136

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Remaining Prior Application data removed - See File Wrapper or PALM. SEQ ID NOS: 160 SOFTWARE: Patentin Ver. 2.1 SEQ ID NO 4 LENGTH: 791
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TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
FILE REFERENCE: 21402-168
CURRENT APPLICATION NUMBER: US/09/981,151A
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Pred. No. 5.5;
1; Mismatches
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PRIOR APPLICATION NUMBER: 60/241,040
PRIOR APPLICATION NUMBER: 60/241,040
PRIOR APPLICATION NUMBER: 60/241,063
PRIOR FILING DATE: 2000-10-17
PRIOR APPLICATION NUMBER: 60/241,063
PRIOR PILING DATE: 2000-10-17
PRIOR PILING DATE: 2000-10-17
PRIOR APPLICATION NUMBER: 60/241,243
PRIOR PILING DATE: 2000-10-23
PRIOR FILING DATE: 2000-10-23
PRIOR FILING DATE: 2000-10-23
PRIOR FILING DATE: 2000-10-24
Sequence 4, Application US/09981151A Publication No. US20030212256A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                            Patturajan, Meera
Taupier Jr, Raymond J
Burgess, Catherine E
Zerhusen, Bryan D
Kekuda, Ramesh
Spytek, Kimberly A
Gangolli, Bsha A
Pernandes, Elma R
                                                                                                                                                                                                                                                                                                      Ellerman, Karen
Shimkets, Richard A
Padigaru, Muralidhara
                                                                                                   Gerlach, Valerie
MacDougall, John R
Malyankar, Muriel M
Smithson, Glennda
Millet, Isabelle
Peyman, John A
Stone, David J
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75.0%;
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Best Local Similarity 75.0
Matches 9; Conservative
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US-09-981-151A-4
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Gaps
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APPLICANT: Gorman, Linda
IITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
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Pred. No. 5.9;
1; Mismatches
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CURRENT APPLICATION NUMBER: US/09/981,151A
CURRENT FILING DATE: 2001-10-16
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PRIOR APPLICATION NUMBER: 60/241,040
PRIOR APPLICATION NUMBER: 60/241,040
PRIOR APPLICATION NUMBER: 60/241,040
PRIOR PILING DATE: 2000-10-17
PRIOR FILING DATE: 2000-10-17
PRIOR FILING DATE: 2000-10-17
PRIOR FILING DATE: 2000-10-17
PRIOR PILING DATE: 2000-10-17
PRIOR PELING DATE: 2000-10-17
PRIOR PELING DATE: 2000-10-23
PRIOR PILING DATE: 2000-10-24
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Sequence 6, Application US/09981151A Publication No. US20030212256Al GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                               Burgess, Catherine E
Zerhusen, Bryan D
Kekuda, Ramesh
Spytek, Kimberly A
Gangolli, Esha A
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Shimkets, Richard A
Padigaru, Muralidhara
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Patturajan, Meera
Taupier Jr, Raymond J
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Gerlach, Valerie
MacDougall, John R
Smithson, Glennda
Millet, Isabelle
Peywan, John A
Stone, David A
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NUMBER OF SEQ ID NOS: 160
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 6
LENGTH: 856
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Best Local Similarity 75.0
Local 9; Conservative
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ORGANISM: Homo sapiens
US-09-981-151A-6
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RESULT 14

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Shimket.

Shimket.

Tr. Galo, Xiaoji Meera

MT: Paupier Jr. Raymond J

ANT: Taupier Jr. Raymond J

ANT: Taupier Jr. Raymond J

ANT: Errubaen, Bryan D

ANT: Spivek, Kinderly A

[CANT: Gangolli, Babha A

LICANT: Gangolli, Babha A

LICANT: Gangolli, Babha A

LICANT: Gangolli, Babha R

RERENTA PAPLICATION NUMBER: 60/241,040

PRIOR APPLICATION NUMBER: 60/241,233

PRIOR PLING DATE: 2000-10-17

PRIOR PLING DATE: 2000-10-17

PRIOR PLING DATE: 2000-10-27

PRIOR APPLICATION NUMBER: 60/242,611

PRIOR APPLICATION NUMBER: 60/242,611

PRIOR PLILANG DATE: 2000-10-23

PRIOR PLILANG DATE: 2000-10-23

PRIOR PLILANG DATE: 2000-10-23

PRIOR PLILANG DATE: 2000-10-24

PRIOR PLILANG DATE: 2000-10-24
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NUMBER OF SEQ ID NOS: 160
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 8
LENGTH: 952
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Pred. No. 6.4;
1; Mismatches 2; Indels
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Best Local Similarity 75.0%;
Matches 9; Conservative
Smithson, Glennda
Millet, Isabelle
Peyman, John A
Stone, David J
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|| || || || || 629 WSSWSPCSRTCG 640
                                                                                                                                Gunther, Erik
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT
; ORGANISM: Homo sapiens
US-09-981-151A-8
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Search completed: April 1, 2005, 14:22:17 Job time : 61.8261 secs

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Sequence 7, Appli
Sequence 4, Appli
Sequence 5, Appli
Sequence 5, Appli
Sequence 5, Appli
Sequence 11, Appl
Patent No. 5426100
Patent No. 5426100
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Appl
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                                                              April 1, 2005, 13:44:22; Search time 21.1304 Seconds (without alignments) 42.393 Million cell updates/sec
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Sequence 1, A
Sequence 3, A
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Sequence 2
Sequence 1
Sequence 1
Sequence 1
Sequence 1
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Sequence 1
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Sequence
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1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/PcTUS_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/PcTUS_COMB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      S-09-825-294-207
S-09-970-966-207
S-07-862-021B-10
S-08-313-288B-10
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US-09-132-769-3
                                                                                                                                                                                              513545 seqs, 74649064 residues
                                                                                                                                                                                                                                                                         Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                             - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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Match Length DB
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77.9
76.6
6.6
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Perfect score:
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                                                                                                                                      Sequence:
                                                                                                                                                                                              Searched:
                                                                   Run on:
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No.
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TYPE: PRT ORGANISM: homo sapiens US-09-930-872-4

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5, Appli 186, App 186, App 186, App 10, Appl 12, Appl 15, Appl 15, Appl 6, Appli 6, Appli 6, Appli 12, Appli 12, Appli 12, Appli 12, Appli 12, Appli 12, Appli 12, Appli			Gaps 0;		les Encoding
Sequence Patent No. Sequence S		Zinc Metalloproteases	Length(997;) ; Indels 0; C		and Polynucleotides
US-09-112-769-5 US-09-113-186 US-09-640-173-186 US-09-173-550-186 US-09-970-966-186 PCT-US93-03164-10 US-09-122-1268-15 US-09-122-1268-15 US-09-134-286A-15 US-09-184-286A-15 US-09-184-286A-15 US-09-184-213-6 US-09-184-213-6 US-09-184-273-6 US-09-197-770B-12 S426100-6 S426100-6 US-09-109-770B-12	ALIGNMENTS	Encoding 0 69,364A	Score 65; DB 3; Pred. No. 2.4; 0; Mismatches 2		Human Proteases 930,872 5,852 ion 4.0
4 4 4 4 4 5 4 4 4 4 4 4 6 6 6 6 6 6 6 6		1,0936 1,11na 1,08hi 1,007/10 1,007/10 1,9-08-10 2.1	4. E	r.	0993 0993 1 US 6 08 6
807 807 807 807 807 1691 1691 233 233 233 60 60		Application US/093693 3931610 389410N: Apte, Suneel Hurskainen, Tiina L. Hirohata, Sacoshi VVENTION: Nucleic Aci NVER 26473/4007/10-3 INCE: 26473/4007/10-3 INCE: 1999-08-06 ENG ID NOS: 31 Patentin Ver: 2.1	e e vatj	WSGWSSCSRSCG 12 	carl Johan Erin No. 644838 0219-USA NUMBER: US NUMBER: US NUMBER: US SOUD-08-16 0000-08-16 0000-08-16 0000-08-16 0000-08-16 0000-08-16 0000-08-16 0000-08-16 0000-08-16 0000-08-16 000000000000000000000000000000000000
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76. 76. 76. 76. 76. 75. 75. 75.		plic pte, wirok Nirok SATI ID A	ilar Cor	SWS AWSI	Applicat: (48388 (48388) (48388) (4810N) (771ddle) (771ddle) (771ddle) (771dle) (7710N)
O O O O O O O O O O O O O O O O O O O		ULT 1 199-369-364A-7 199-369-364A-7 199-364-7 199-36-7 199-391610 199-391610 199-30-30-30-30-30-30-30-30-30-30-30-30-30-	တ္မ	1 WS(ULT 2 09-930-872-4 equence 4, Application US/09930872 lequence 4, Application US/09930872 learent No. 6448388 APPLICANT: Friddle, Carl Johan APPLICANT: Hilbun, Erin TITLE OF INVENTION: 64483881 FILE REFERENCE: LEX-0219-USA CURRENT FILING DATE: 2001-08-14 PRIOR FILING DATE: 2001-08-14 PRIOR FILING DATE: 2001-08-14 PRIOR FILING DATE: 2000-08-16 NUMBER OF SEQ ID NOS: 5 SOFTWARKE: PastSEQ for Windows Vere SEQ ID NO 4 TYPE: PRT
00000000000000000000000000000000000000		RESULT 1 US-09-369-364A-7 Sequence 7, Application US/09369364A Patent No. 6391610 FARERAL INFORMATION: APPLICANT: Apte, Suneel APPLICANT: Hurshata, Satchin, TITLE OF INVENTION: Nucleic Acids FILE REFERENCE: 26473/407/10-30-0 CURRENT APPLICATION NUMBER: US/09/3 CURRENT APPLICATION NUMBER: US/09/3 CURRENT FILING DATE: 1999-08-06 NUMBER OF SEQ ID NOS: 31 SOFTWARE: PatentIN Ver. 2.1 SSOFTWARE: PatentIN Ver. 2.1 TYPE: PRT TYPE: PRT CURRENTH HOMO SADIENS ADAMTS-7 US-09-369-364A-7	Query Match Best Local Similarity Matches 10; Conser	op ox	NESULT 2 Sequence 4, Application US/09930872 Sequence 4, Application US/09930872 Patent No. 6448388 GENERAL INFORMATION: APPLICANT: Fitiable, Carl Johan APPLICANT: Hilbun, Erin TITLE OF INVENTION: 644838e1 FILE REPERENCE: LEX-0219-USA CURRENT FILING DATE: 2001-08-14 PRIOR FILING DATE: 2001-08-14 PRIOR FILING DATE: 2000-08-16 NUMBER OF SEQ ID NOS: 5 SOFTWARE: PastSEQ for Windows Vers SEQ ID NO 4 ILENGTH: 1224 TYPE: PRI

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GENERAL INFORMATION:

APPLICANT: Delucch, Alan H.

APPLICANT: Delucch, Alan H.

APPLICANT: TUSZYISKI, GEOTGE P.

TITLE OF INVENTION: THEOMBOSPONDIN

NUMBER OF INVENTION: THEOMBOSPONDIN

NUMBER OF SEQUENCES: 15

CORRESPONDENCE ADDRESS:

ADDRESSE: ADDRESS: 15

CORRESPONDENCE ADDRESS:

ADDRESSE: ADDRESS: 1601 Market Street, 36th Floor

CITY: Philadelphia

STREET: 1601 Market Street, 36th Floor

CITY: Philadelphia

STREET: 19103-2398

COMPUTER: READABLE FORM:

MEDIUM TYPE: Floppy disk

MEDIUM TYPE: Floppy disk

MEDIUM TYPE: Floppy disk

MEDIUM TYPE: PLOPS/MS-DOS

COMPUTER: IBM PC compatible

COMPUTER
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                                                                                                                                                                                                                                                                                                                                                            1; Mismatches
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Sequence 5, Application US/08488273;
Patent No. 5840692
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TELECOMMUNICATION INFORMATION
TELEPHONE: (215) 567-2020
                                                                                                                                                                                                                                                                                            77.9%;
75.0%;
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 23 amino acids
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Best Local Similarity 75.0
Matches 9; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                        1 WSGWSSCSRSCG 12
                                                                                                             TYPE: AMINO ACID
TOPOLOGY: linear
MOLECULE TYPE: peptide
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; Sequence 4, Application US/1021774
; Sequence 4, Application US/1021774
; Patent No. 6734007
; GENERAL INFORMATION:
    APPLICANT: Friddle, Carl Johan
; APPLICANT: Hibbut, Erin
    TITLE OF INVENTION: Same
; PRIOR FILING DATE: 2001-08-14
; PRIOR FILING DATE: 2000-08-16
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 1224
; TITLE OF INVENTION: Same
; TITLE OF INVENTION
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               Score 63; DB 4; Length 1224;
Pred. No. 4.9;
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Sequence 5, Application US/07646531D
Patent No. 5200397
Fatent No. 5200397
JERRAL INFORMATION:
APPLICANT: Deutch, Alan Howard
APPLICANT: Tusynski, George Paul
TITLE OF INVENTION: Peptide Fragments and Analogs of
TITLE OF INVENTION: Thrombospondin
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: W. R. Gazee & Co.-Conn.
STREET: 7379 Route 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2; Indels
                                                                                          2; Indels
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COMPUTER: IBW PC compatible
COMPUTER: IBW PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 5.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/646,531D
FILING DATE: 19910131
ATTORNEY/AGENT INFORMATION:
NAME: APPLED, Vanessa 1.
REGISTRATION NUMBER: 33223
REGISTRATION NUMBER: 33223
REPERSINGE/DOCKET NUMBER: 01-7896
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 531-4515
                          81.8%;
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CITY: Columbia
STATE: Maryland
COUNTRY: USA
ZIP: 21044
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy di
COMPUTER: IBM PC comps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity 75.0
Matches 9; Conservative
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                                                            Best_Local Similarity 75.0
Matches 9; Conservative
                                                                                                                                                                          1 WSGWSSCSRSCG 12
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ORGANISM: homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 4
US-07-646-531D-5
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US-10-217-774-4
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TITLE OF INVENTION: PIPTIDE FRAGMENTS AND ANALOGS OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     19899
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-08-985-526-1
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                                                                                                                                                                    Sequence 11, Application US/09197770B
Patent No. 6339062
JERERAL INPORMATION:
APPLICANT: TUSZYMSKI, George
APPLICANT: Williams, Taffy
APPLICANT: Williams, Taffy
ITILE OF INVENTION: RETROINVERSO POLYPEPTIDES THAT MIMIC OR INHIBIT
ITILE OF INVENTION: THROMBOSPONDIN ACTIVITY
ITILE OF INVENTION: THROMBOSPONDIN ACTIVITY
ITILE OF INVENTION: THROMBOSPONDIN ACTIVITY
CURRENT APPLICATION NUMBER: US/09/197,770B
CURRENT PELLING DATE: 1998-11-23
NUMBER OF SEQ ID NOS: 38
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 11
LENGTH: 23
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                      Gaps
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Jatent No. 5426100
Jatent No. 5426100
Jatent No. 5426100
JAPLICANT: DEUTCH, ALAN H.;TUSZYNSKI, GEORGE
JILLE OF INVENTION: PIPTIDE FRAGMENTS AND ANALOGS OF
J. THROWHOSPONDIN
NUMBER OF SEQUENCES: 12
CURRENT APPLICATION DATA:
JELING DATE: 20-AUG-1993
JERIOR APPLICATION DATA:
JAPLICATION NUMBER: 896,527
FILING DATE: 09-JUN-1992
JELING DATE: 22-FEB-1990
JELING DATE: 22-FEB-1990
                    2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2; Indels
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 Pred. No. 0.39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    77.9%; Score 60; DB 75.0%; Pred. No. 0.39:ive 1; Mismatches
                    1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT
ORGANISM: Artificial Sequence
75.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 75...
Best Local Similarity 75...
Best Local Similarity 75.0
Matches 9; Conservative
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Matches 9; Conservative
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                                                    1 WSGWSSCSRSCG 12
                                                                         4 WSEWTSCSTSCG 15
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                                                                                                                                          RESULT 6
US-09-197-770B-11
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5426100-5
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Sequence 1, Application US/0898526
Patent No. 680728
GENERAL INFORMATION:
APPLICANT: MIXSON, James A
TITLE OF INVENTION: CARRIER: DNA COMPLEXES CONTAINING DNA
TITLE OF INVENTION: THERAPY
NUMBER OF SEQUENCES: 43
CORRESPONDENCE ADDRESS:
ADDRESSEE: Connolly, Bove, Lodge, & Hutz
                                                                                                                                                                                                                                                                                                                                ö
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Pred. No. 2.6;
1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                      Score 60; DB 6; Length 23;
Pred. No. 0.39;
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PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                iE: Connolly, Bove, Lodge, & Hutz
1220 Market Street, P.O. Box 2207
THROMBOSPONDIN

UUMBER OF SEQUENCES: 12

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/110,146

FILING DATE: 20-AUG-1993

PRIOR APPLICATION DATE: 895,527

FILING DATE: 09-UUN-1992

APPLICATION NUMBER: 483,527

FILING DATE: 22-FEB-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/608,845
FILING DATE: 16-JUL-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/985,526
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: MCMOITOW Jr., Robert G
TELECOMMUNICATION INFORMATION:
TELEPHONE: (302) 658-9141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                        77.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            77.9%;
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INFORMATION FOR SEQ ID NO: 1:
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                                                                                                                                                                                                                                                                                        Query Match 77.9
Best Local Similarity 75.0
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                        1 WSGWSSCSRSCG 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 77.5
Best Local Similarity 75.0
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 WSGWSSCSRSCG 12
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85 WSEWTSCSTSCG 96
                                                                                                                                                                                                                                                                                                                                                                                                             4 WSEWTSCSTSCG 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CITY: Wilmington
STATE: Delaware
COUNTRY: U.S.A.
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Delaware

STATE:

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Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       77.9%; Score 60; DB 3; Length 441; 75.0%; Pred. No. 4.7; 2; Indels :ive 1; Mismatches 2; Indels
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                 CIP: 19899
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPATING SYSTEM: PC-DOS/MS-DOS
SOUTHARE: PatentIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/985,526
FILING DATE:
FILING DATE: 16-JUL-1996
ATTORNEY/AGENT INFORMATION:
MAME: MCMORTOW JT., ROBERT G
FILING DATE: 16-JUL-1996
ATTORNEY/AGENT INFORMATION:
MAME: MCMORTOW JT., ROBERT G
FILING TO 102) 658-9141
TELEFRAN: (302) 658-9141
TELEFRAN: (302) 658-9141
TELEFRAN: (302) 658-9141
TELEGTH: 441 amino acide
JTYPE: amino acid
TOPOLOGY: linear
US-08-985-526-3
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; Sequence 217 Application US/09800729
; Patent No. 660552
; GENERAL INFORMATION:
; APPLICANT: Ni et al.
; TITLE OF INVENTION: 32 Human secreted proteins
; TITLE OF INVENTION: 32 Human secreted proteins
; CURRENT APPLICATION NUMBER: US/09/800,729
; CURRENT PILING DATE: 2001-03-08
; PRIOR PILING DATE: 2001-03-08
; PRIOR FILING DATE: 1999-09-24
; NUMBER OF SEQ ID NOS: 217
; SCFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 217
; SEQ ID NO 217
; LENGTH: 1059
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-800-729-217
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; Sequence 10. 5780502
; GENERAL INFORMATION:
; APPLICANT: Jessell, Thomas M. and Avihu Klar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
77.9%; Score 60; DB
Best Local Similarity 66.7%; Pred. No. 9.9;
Matches 8; Conservative 3; Mismatches
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Best Local Similarity 75.0
Matches 9; Conservative
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85 WSEWTSCSTSCG 96
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U.S.A.
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Sequence 3, Application US/08985526

Patent No. 6080728

GENERAL INFORMATION:
APPLICANT: Mixson, James A
TITLE OF INVENTION: ENCODING ANTI-ANGIOGENIC PEPTIDES AND THEIR USE IN GENE
TITLE OF INVENTION: THERAPY
NUMBER OF SEQUENCES: 43
CORRESPONDENCE ADDRESS:
ADDRESSEE: Connolly, Bove, Lodge, & Hutz
STREET: 1120 Market Street, P.O. Box 2207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaрв
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY: USA

ZIP: 6066-4002

ZIP: 6066-4002

COMPUTER: USA

COMPUTER: Floppy disk

COMPUTER: Floppy disk

COMPUTER: PR PC compatible

COMPUTER: PATEN: PC-DOS/MS-DOS

SOFTWARE: PATENTIN SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PATENTIN PATA:

APPLICATION:

APPLICATION:

CURSIFICATION:

CLASSIFICATION:

                                                          Sequence 1, Application PC/TUS9301652
Sequence 1, Application PC/TUS9301652
GENERAL INFORMATION:
APPLICANT: Bouck, Noel P.
APPLICANT: Good, Deborah J.
APPLICANT: Frazier, William A.
ITILE OF INVENTION: Method and Composition for TITLE OF INVENTION: Inhibiting Angiogenesis NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Tilton, Fallon, Lungmus & Chestnut STREET: 100 South Wacker Drive, Suite 960
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: Connolly, Bove, Lodge, & Hutz
STREET: 1220 Market Street, P.O. Box 2207
CITY: Wilmington
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PRICKATION NUMBER: US/07/841,656
PRICKATION NUMBER: US/07/841,656
PRICKATION DATA:
PRICKATION DATA:
APPLICATION NUMBER: US/07/464,369
FILING DATE: 12-JAN-1990
ATTORNEY/AGENT INFORMATION:
NAME: Featress, Susan B.
REGISTRATION NUMBER: 31,327
REGISTRATION NUMBER: 31,327
REFERENCE/DOCKET NUMBER: 92005-PCT
TELEPHONE: (312)-456-8000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 60;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: (312)-456-776
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERLETICS:
LENGTH: 239 amino acids
TYPE: AMINO ACID
STRANDEDNESS: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       77.98;
75.08;
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MOLECULE TYPE: peptide
PCT-US93-01652-1
                                                                                                                                                                                                                                                                                                                                                                                                                    ADDA.
STREET: loc
CITY: Chicago
                                                          PCT-US93-01652-1
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APPLICANT: Cargill, Michele
APPLICANT: Cargill, Michele
APPLICANT: Targill, Michele
APPLICANT: Bolk, Stacey
APPLICANT: Bolk, Stacey
APPLICANT: Bolk, Stacey
APPLICANT: Bolk, Stacey
APPLICANT: Michele
TITLE OF INVENTION: SINGLE WUCLEOTIDE POLYMORPHISMS IN GENES
FILE REFERENCE: 2825.1027-001
CURRENT FILING DATE: 2000-09-07
PRIOR APPLICATION NUMBER: US 60/153,357
PRIOR APPLICATION NUMBER: US 60/153,357
PRIOR PILING DATE: 2000-09-07
PRIOR PILING DATE: 2000-07-26
PRIOR PILING DATE: 2000-07-26
PRIOR PILING DATE: 2000-08-16
NUMBER OF SEQ ID NOS: 2551
SOSTWARE: PSELSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 60; DB 1; Length 1170;
Pred. No. 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2; Indels
TITLE OF INVENTION: CLONING, EXPRESSION AND USES OF A TITLE OF INVENTION: NOVEL SECRETED PROTEIN, F-SPONDIN NUMBER OF SEQUENCES: 20
AUTHERSPONDENCE ADDRESS: ADDRESS: ADDRESS: Cooper & Dunham LLP STREET: 1185 Avenue of the Americas
                                                                                                                                                                                                             COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

MEDIUM TYPE: Ploppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/313,288B

FILING DATE: January 5, 1995

CLASSIFICATION: 435

ATORNEY/AGENT INFORMATION:

NAME: White, John P.

REGISTRATION NUMBER: 28,678

REGISTRATION NUMBER: 28,678

REGISTRATION NUMBER: 28,678

REGISTRATION NUMBER: 28,678

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

TELEFRAX: (212) 278-0400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 2, Application US/09657472
Patent No. 6727063
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 1170 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 75.0
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  385 WSEWTSCSTSCG 396
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; TOPOLOGY: linear;
; MOLECULE TYPE: peptide
US-08-313-288B-20
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; ORGANISM: Homo sapiens
US-09-657-472-2
                                                                                                                                               CITY: New York
STATE: New York
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: amino acid
STRANDEDNESS: si
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQ ID NO 2
LENGTH: 1170
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Score 60; DB 4; Length 1170;
Pred. No. 11;
                                                                                                                                                                                                              Sequence 12, Application US/08799173A
; Sequence 12, Application US/08799173A
; Patent No. 581269
; GENERAL INFORMATION:
    APPLICANT: HASTINGS, GREGG,
; TITLE OF INVENTION: HUMAN NEURONAL ATTACHMENT FACTOR-1
NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; STREET: 9410 KEY WEST AVENUE
; CITY: ROCKVILLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 59; DB 2; Length 52;
Pred. No. 1;
2; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY: ....
ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/799,173A
FILING DATE: 11-FEB-1997
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: BROOKEZ, ANDERS, A.
REFERENCE/DOCKET NUMBER: 36,373
REFERENCE/DOCKET NUMBER: 36,373
REFERENCE/OOKET NUMBER: PF226
TELECOMMUNICATION INFORMATION:
TRIEDFONE: (301) 309-8504
                                           1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Search completed: April 1, 2005, 14:01:57 Job time: 21.1304 secs
77.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: (301) 309-8512
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 52 amino acids
                                                                                                                       385 WSEWTSCSTSCG 396
Query Match
Best Local Similarity 75.0
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 76.6
Best Local Similarity 66.7
Matches 8; Conservative
                                                                                1 WSGWSSCSRSCG 12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      , MOLECULE TYPE: protein US-08-799-173A-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRANDEDNESS:
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ii iis rage biatik (uspiu)

GenCore version 5.1.6 Copyright (c) 1993 - 2005 Compugen Ltd.

- protein search, using sw model OM protein April 1, 2005, 13:22:55 ; Search time 83.7391 Seconds (without alignments) 55.424 Million cell updates/sec Run on:

US-09-462-909D-8

1 WSGWSSCSRSCG 12 score: Sequence: Perfect

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

2105692 segs, 386760381 residues Searched:

2105692 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

A_Geneseq_16Dec04:* Database

geneseqp2000s:* geneseqp2001s:* geneseqp2002s:* geneseqp2003as:* geneseqp2003bs:* geneseqp2004s:* geneseqp1980s:* geneseqp1990s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	Aaw97445 Peptide t	_		Adh48718 NOV1 prot	Nove	Adn95228 Human BEC	Abg21064 Novel hum	Aab72283 Human ADA	Adj69288 Human hea	Abb60410 Drosophil	Adi28031 ECMCAD pr	Aae00934 Human 278	Aae00913 Human 278	Aab74944 Human ADA	Adj58902 Human ADA	Aab86949 Human met	Aab41379 Human ORF	Abj19383 NOVX rela	Nove]	Abg31503 Human ADA	Abr58452 Human NOV	Abr58460 Human NOV	Ada50469 Human pro	Abg76895 Human zin	Adj38422 Human nov
SUMMARIES	ID	AAW97445	ADP04709	ABU62079	ADH48718	ABG30203	ADN95228	ABG21064	AAB72283	ADJ69288	ABB60410	ADI28031	AAE00934	AAE00913	AAB74944	ADJ58902	AAB86949	AAB41379	ABJ19383	AD041766	ABG31503	ABR58452	ABR58460	ADA50469	ABG76895	ADJ38422
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ď	Query	100.0		. 88	88.3	88.3	88.3	88.3	84.4	84.4	84.4	84.4	84.4	84.4	84.4	84.4	84.4	84.4	83.1	83.1	81.8	81.8	81.8	81.8	81.8	81.8
	Score	77	89	68	68	68	68	68	65	65	65	65	65	65	65	65	65	65	64	64	63	63	63	63	63	63
	Result No.	-	7	m	4	·w	9	7	80	σ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25

Abg76896 Human ADA Adj38424 Human nov Abg76897 Human ADA Adj38426 Human ADA Adj38426 Human zin Adj38420 Human zin Adj38420 Human par Abau79496 Human par Abau79500 Human ADA Aau79570 Human MDA Aau7957 Human MDA Aau79497 Human MDT Aau79497 Human MDT Aau79497 Human MDT Aau79497 Human ADA Aau79497 Human ADA Aau79497 Human ADA Aau80153 Human ADA	Abg72431 Novel hum Abr8432 Human ADA Ada50762 Novel hum Abm79745 Human pro Aau9886 Human pro Abm84501 Human dia
ABG76896 ADJ38424 ADD38424 ADR09503 ADG76897 ADJ38426 AAUT9496 AAUT9500 AAUT9500 AAUT9500 AAUT9500 AAUT9500 AAUT9891 AAUT9891 AAUT9891	ABG72431 ABR83432 ABA70762 ABM79745 AAU9886
α_{L}	928499
856 856 958 952 952 986 1021 1170 1224 1224 1224	1224 1224 1224 1224 1236
81.38 81.38 81.38 81.38 81.38 81.38 81.38	81.8 81.8 81.8 81.8 81.8
	999999
0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	4 4 4 4 4 0 4 5 6 4 5

ALIGNMENTS

AAW97445 standard; peptide; 12 AA. (first entry) 19-MAY-1999 AAW97445; RESULT 1 AAW97445

Peptide that is useful for regenerating the nervous system.

Neuronal sprouting; cerebral cortex; spinal cord cell; aggregation; neurite defasiculation; regeneration; nervous system cell; nerodegenration; Alzheimer's; Parkinson's disease; multiple sclerosis; myopathy; synapse formation; neuroblastoma.

Synthetic.

WO9903890-A1

28-JAN-1999.

98WO-FR001556, 16-JUL-1998; 97FR-00009016. 16-JUL-1997;

(UYAU-) UNIV AUVERGNE.

Gobron S; Monnerie H, Meiniel A,

New polypeptides for promoting growth of neurons - useful for treatment of neurodegeneration, neuroblastoma and as additives for neuronal cell WPI; 1999-132166/11.

Claim 6; Page 14; 29pp; French.

cultures.

The present sequence represents a peptide that stimulates neuronal (particularly axonal) sprouting in neurons of the cerebral cortex, and in spinal cord cells inhibits aggregation and defasiculation of neurites while increasing formation of synaptic contacts. The peptide is used to regenerate nervous system cells, particularly for treating neurodegeneration (e.g. Alzheimer's or Parkinson's diseases, multiple sclerosis and myopathy), other conditions requiring regeneration (particularly elongation and synapse formation) or neuroblastoma. The peptide can also be used as an additive for neuronal cell cultures

Sequence 12 AA;

Human, jelly belly protein, jeb; visceral mesoderm migration, differentiation; neuron; late embryogenesis; LDL receptor repeat; development of nervous system; low density lipoprotein receptor; hyperproliferative disorder; atherosclerosis; antiarteriosclerotic.

06-AUG-2002; 2002US-00213509 09-AUG-2001; 2001US-0311720P.

US2003054485-A1.

20-MAR-2003

Homo sapiens.

Weiss JB;

Scott MP,

ч ч

(SCOT/) SCOTT M (WEIS/) WEISS J

WPI; 2003-540614/51

Human jelly belly (jeb) protein.

(first entry)

16-SEP-2003

ABU62079 standard; protein; 4123 AA.

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This invention relates to novel genes and the encoded proteins thereof
that are derived from the sea squirt Ciona intestinalis. Specifically, it
refers to those genes that are expressed in the tissues or organs of the
sea squirt during its developmental phase. The present invention
describes the identification of these genes as useful for elucidation of
the mechanism of development and hence for developing regeneration
the mechanism of development and hence for developing regeneration
the research of various genetic diseases, as well as the analysis of cell
the research of various genetic diseases, as well as the analysis of cell
compositions can be useful for environmental measurements and water
surveys, particularly for sea water surveys, and also for the preparation
of transformed sea squirt for improving edibility of sea squirt such as
Halocynthia roretzi. This polypeptide sequence is a sea squirt protein
sequence that has tissue specific expression during development, given in
                                       ö
                                                                                                                                                                                                                                                                                                                  Sea squirt protein with tissue specific expression in development Seq304.
                                                                                                                                                                                                                                                                                                                                                       sea squirt; regeneration medicine; gene therapy; cell proliferation;
differentiation; reproduction; environmental measurement; water survey.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Novel gene cluster which is specifically expressed in tissue or organ during developmental phase of sea squirt, useful for elucidation of mechanism of development of tissue or organ of sea squirt.
                                       Gaps
                                       ;
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Pred. No. 0.85;
1; Mismatches 1; Indels
100.0%; Score 77; DB 2; Length 12; 100.0%; Pred. No. 0.0019; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 1; SEQ ID NO 304; 1846pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN
                                                                                                                                                                                                            ADP04709 standard; protein; 606 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                31-JUL-2002; 2002JP-00222593.
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Best Local Similarity 83.3%;
Matches 10; Conservative
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                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                 1 WSGWSSCSRSCG 12
                                           12, Conservative
                                                                              1 WSGWSSCSRSCG 12
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                                                                                                                                                                                                                                                                                                                                                                                                                      Ciona intestinalis.
                       Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            JP2004057129-A.
                                                                                                                                                                                                                                                                                       29-JUL-2004
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                                                                                                                                                                                                                                                   ADP04709;
       Query Match
Best Local 9
                           Best Loc
Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                 melanogaster) jelly belly (jeb) protein, and the polymucleotide sequence encoding it. Jeb is required for visceral mesoderm migration and edifferentiation. Jeb is expressed in neurons in late embryogenesis indicating that it may play a role in the development of the nervous system. The jeb protein contains a LDL (low density lipoprotein) receptor repeat. The polymucleotide sequence encoding jeb is useful for preparing a composition for treating hyperproliferative disorders such as atherosclerosis. The present sequence represents human jeb protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human; NOVX; atherosclerosis; hypertension; obesity; cancer; cytostatic;
hypotensive; antiarteriosclerotic; anorectic; gene therapy; NOV1;
DJ0751H13.1 protein-like protein; chromosome 8.
                                                                                                                                                                                                                                                                                                                                                                                                                        The present invention relates to the isolation of fruitfly (Drosophila
                                                                                                                                                                                                                                                                                                                                                             New jelly belly gene, useful for preparing a composition for treating hyperproliferative disorders e.g., atherosclerosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure; Page 18-28; 40pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADH48718 standard; protein; 4219 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NOV1 protein sequence, SEQ ID 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          88.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2518 WSVWSSCSRSCG 2529
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 91...
Pest Local 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 WSGWSSCSRSCG 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 4123 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 4
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Gaps

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1:|||||| ||| 257 WTGWSSCSASCG 268

RESULT 3 ABU62079

1 WSGWSSCSRSCG 12

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New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
                                                                                                                                                                                                                                     Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder.
                                                                                                                                                                                    Novel human diagnostic protein #30194.
                                                  ABG30203 standard; protein; 4561 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                               30-MAR-2001; 2001WO-US008631
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             31-MAR-2000; 2000US-00540217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   23-AUG-2000; 2000US-00649167
                                                                                                                                         18-FEB-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Drmanac RT, Liu C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2001-639362/73.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                N-PSDB; AAS94390
                                                                                                                                                                                                                                                                                                                                                    WO200175067-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 biodiversity.
                                                                                                                                                                                                                                                                                                           Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                  11-OCT-2001.
                                                                                              ABG30203;
    RESULT 5
                            ABG30203
                                                                                              The present invention relates to novel human NOVX proteins, where x is any number from 1 to 91 and their coding sequences. The proteins and coding sequences are useful for preventing or treating disorders or syndromes e.g. atherosclerosis, hypertension, obseity or cancer. NOV1 is a DJ0751H13.1 protein-like protein and its coding sequence maps to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Stone DJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Peyman JA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Alsobrook JP, Anderson DW, Ballinger RA, Boldog FL, Burgess CE; Casman SJ, Ellerman KE, Gangolli EA, Gerlach VL, Gilbert JA; Gorman L, Guo X, Gusev VY, Kekuda R, Li L, Liu X, Malyankar UM; Miller CE, Millet I, Padigaru M, Patturajan M, Pena CEA, Peyman J Rastelli L, Shenoy SG, Shinkets RA, Smithson G, Spytek KA, Stone Taupier RJ, Tchernev VT, Vernet CAM, Zerhusen BD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New NOVX polypeptides or polynucleotides, useful for preventing or treating disorders or syndromes e.g., atherosclerosis, hypertension
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 1; Page 13-14; 923pp; English.
                                                                                                                             27-FEB-2001; 20010S-0271640P.
28-FEB-2001; 2001US-0271404P.
28-FEB-2001; 2001US-0272404P.
28-FEB-2001; 2001US-0272404P.
28-FEB-2001; 2001US-0272410P.
28-FEB-2001; 2001US-0272414P.
02-MAR-2001; 2001US-027324P.
02-MAR-2001; 2001US-027324P.
16-MAR-2001; 2001US-027324P.
20-MAR-2001; 2001US-027324P.
20-MAR-2001; 2001US-0276401P.
20-MAR-2001; 2001US-0278660P.
30-MAR-2001; 2001US-028603P.
30-MAR-2001; 2001US-0280033P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          03-MAY-2001, 2001US-0288353P.
17-MAY-2001, 2001US-0291703P.
31-MAY-2001, 2001US-0294834P.
20-JUN-2001, 2001US-029695P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   21-JUN-2001; 2001US-0299845P.
05-JUL-2001; 2001US-0303242P.
13-AUG-2001; 2001US-0311981P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           12-APR-2001; 2001US-0283443P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            23-APR-2001; 2001US-0285754P. 24-APR-2001; 2001US-0286096P.
                                                                   26-FEB-2002; 2002WO-US005910
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2002-698672/75
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 4219 AA;
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                        06-SEP-2002
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$\frac{1}{2} \frac{1}{2} \frac
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Tang YT;

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The invention relates to isolated polymucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain creation (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polymucleotides are also used in diagnostics as expressed sequence tags for identifying expressed considerable (II) as useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is cuspilement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and its binding partners are useful in medical imaging of sites expressing (II). (II) and its binding partners are useful in medical imaging of sites expressing (II). (II) and its binding partners are useful for treating disorders (I) polypeptide and polymucleotide sequences have applications in casponsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and and can appear and the printed specification, but was obtained in calestronic format directly from WHDO at the wipe of the printed specification, but was obtained in the wip int, pub/published_pot_sequences
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 68; DB
Pred. No. 5;
0; Mismatches
Claim 20; SEQ ID NO 60562; 103pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 91.7%;
Matches 11; Conservative
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RESULT 6 ADN95228

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Gaps

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Local Similarity 91.7 es 11,7 Conservative 1 WSGWSSCSRSCG 12

Best Loca Matches

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Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder.

Novel human diagnostic protein #21055.

(first entry)

18-FEB-2002

ABG21064;

RESULT 7

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ADN95228 standard; protein; 5737 AA
                                                                                                                   80.3
Best Local Similarity 91.7
Matches 11; Conservative
       01-JUL-2004
                                02-OCT-2003.
    ADN95228;
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ABG21064 standard; protein; 9222 AA.
ABG21064
                                              This invention relates to a method of differentially modulating the growth or differentiation of blood endothelial cells (BEC) or lymphatic growth or differentiation of blood endothelial cells with a candothelial cells (LEC) comprises contacting endothelial cells with a composition comprising an agent that differentially modulates blood or composition comprises. Treating hereditary lymphoedema comprises identifying a human subject with lymphoedema and with a mutation in at correlates with lymphoedema in human subjects, and with the proviso that correlates with lymphoedema in human subjects, and with the proviso that correlates with lymphoedema in human subjects, and with the proviso that correspond a lymphatic growth agent selected from VEGF-C or VEGF-D polypeptides and polymucleotides. The invention may be useful in comprising a lymphatic growth agent elected from VEGF-C or vasotropic or antiinflammatory activity or for gene therapy. The method is useful in modulating the growth or differentiation of blood endothelial cells or lymphatic endothelial cells, in treating hereditary lymphoedema, in screening for an endothelial cells, in treating hereditary predisposition to the disorder or in monitoring the efficacy or toxicity of a drug on endothelial cells. The agent is useful in manufacturing a medicament for the differential modulation of blood vessel endothelial cells growth agent may also be used in manifacturing a meticament of hereditary lymphoedema resulting from a mutation in a the treatment of hereditary lymphoedema resulting from a mutation in a LEC gene or of other diseases involving the lymphatic vessels, such as LEC gene or of other diseases involving the lymphatic vessels, such as LEC gene or of other diseases involving the lymphatic vessels, such as LEC gene or of other diseases and cancer metastasis via the lymphatic system. The present sequence is that of a human LEC/BEC differential or any also be expressed protectin which is related to the method of the involving hypatics.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This sequence does not appear in the specification but was obtained by the indexer using the source data given in table 14 of the specification.
                                                                                                                                               growth; differentiation; blood endothelial cell; BEC; lymphatic endothelial cell; LEC; hereditary lymphoedema; VEGFR-3; lymphatic growth agent; VEGF-7; VEGF-D; antiangiogenic; cytostatic; vasotropic; antiinflammatory; gene therapy; endothelial cell disorder; inflammatory disease; cancer metastasis; lymphatic system; human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Petrova T, Saharinen P, Saharinen J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 7; Length 5737;
                                                                                                       Human BEC/LEC-related protein sequence SeqID150.
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91.7%; Pred. No. 6.1;
:ive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Example 1; SEQ ID NO 150; 176pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (LUDW-) LUDWIG INST CANCER RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       07-MAR-2003; 2003WO-US006900.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              07-MAR-2002; 2002US-0363019P.
                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Alitalo K, Makinen T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (LICN ) LICENTIA LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2003-876899/81.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         N-PSDB; ADN95229
                                                                                                                                                                                                                                                                                                                                                                           WO2003080640-A1.
                                                                                                                                                                                                                                                                                                                             Homo sapiens
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New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess

31-MAR-2000; 2000US-00540217. 23-AUG-2000; 2000US-00649167. 30-MAR-2001; 2001WO-US008631.

WO200175067-A2.

11-OCT-2001.

Homo sapiens.

Tang YT;

Drmanac RT, Liu C,

(HYSE-) HYSEQ INC

WPI; 2001-639362/73.

N-PSDB; AAS85251

Claim 20; SEQ ID NO 51423; 103pp; English.

biodiversity.

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The invention relates to isolated polymucleotide (I) and polypeptide (II) capenose. (I) is useful as hybridisation probes, polymerase chain sequences. (I) is useful as hybridisation probes, polymerase chain recombinant production of (II). The polymucleotides are also used in diagnostics as expressed sequence tags for identifying expressed conditions useful in gene therapy techniques to restore normal cativity of (II) or to treat disease states involving (II). (II) is useful in gene therapy techniques to restore normal cativity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a useful for generating antibodies against it, detecting or quantitating of supplement. (I) and its binding partners are useful in medical imaging of sites expressing (II). (II) and (II) are useful for treating disorders of sites expressing (II). (II) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The involving and polymucleotide sequences have applications in diagnostics, for genefic disorders or other trails to assess biodiversity responsible for genefic disorders or other trails to assess biodiversity amino acid sequences of the invention. Note: The sequence data for this amino acid sequences of the invention. Note: The sequence data for this electronic format directly from WIPO at certical control format directly from WIPO at
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91.7%; Pred. No. 9.2;
iive 0; Mismatches
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Best Local Similarity
Matches 11; Conserv
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œ RESULT

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Gaps ö

Indels

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3022 WSVWSSCSRSCG 3033

셤 à

1 WSGWSSCSRSCG 12

Huntington's disease; osteoarthritis; Leber's hereditary optic neuropathy; LHON; micochondrial encephalopathy lactic acidosis and stroke; MELAS; mycolonic epilepsy ragged red fibre syndrome; MERRF; cancer; neuroprotective; nootropic; antidiabetic; anticonvulsant; antiarthritic; osteopathic; ophthalmological; cytostatic.

Human heat mitochondrial protein as a therapeutic target SeqID1094

06-MAY-2004 (first entry)

mitochondrial; human; screening assay; diabetes mellitus;

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This invention relates to murine and human ADAWTS-N (A disintegrin-like and metalloprotease domain with thrombospondin type I motifs) proteins, designated ADAWTS-5, 6, 7, 8, 9, 10 and R1. Also included in the invention are cDNA sequences encoding the proteins, and antibodies specific for the proteins. The nucleic acid sequences and proteins may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate ADAMTS-N expression. Disorders that may be treated using the nucleic acids, proteins and antibodies include, for example tumour cachexia, inflammation, dermatosparaxis in cattle or Ehlers-Danlos syndrome type VIIC (EDS-VIIC) in humans, erosion of articular cartilage in arthritic (both inflammatory) disease.

Cangiogenesis, tumour growth and metastases, and they may also be used for controlling embryogenesis and implantation of fertilised eggs. The present sequence represents human ADAMTS-7. The human ADAMTS-7 gene is
                                                                                                                                                     ADAMTS-N; disintegrin; metalloprotease; thrombospondin type I motif; tumour cachexia; inflammation; dermatosparaxis; BDS-VIC; angiogenesis; Ehlers-Danlos syndrome type VIIC; articular cartilage erosion; human; metastasis; embryogenesis; egg implantation; chromosome 15; ADAMTS-7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Murine and human 'A Disintegrin-like And Metalloprotease domain with ThromboSpondin type I motifs' proteins and the nucleic acids encoding them, useful for treating e.g. tumors, inflammation and arthritis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hirohata S;
                                                                                                                      Human ADAMTS-7 amino acid sequence.
                AAB72283 standard; protein; 997 AA
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                                                                                                                                                                                                                                                                                                                                                 03-AUG-2000; 2000WO-US021223.
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83.3%;
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Bust Local Similarity 83.39,
                                                                                  (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     HURSKAINEN T L.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HIROHATA S.
                                                                                                                                                                                                                                                                                                                                                                                                                                       APTE S S.
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                                                                                                                                                                                                                                             Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                 06-AUG-1999;
                                                                                    14-MAY-2001
                                                                                                                                                                                                                                                                                                              15-FEB-2001.
                                                  AAB72283
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(HURS/)
(HIRO/)
                                                                                                                                                                                                                                                                                                                                                                                                                     CLEV-)
AAB72283
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Identifying a mitochondrial target for drug screening assays and for treating diseases associated with altered mitochondrial function, comprises detecting a modified polypeptide in a sample and correlating

Claim 1; SEQ ID NO 1094; 180pp; English.

with the disease.

Glenn GM

Taylor SW,

Gibson BW,

Zhang B,

Fahy ED,

Warnock DE; SS,

Ghosh

WPI; 2003-845369/78.

12-APR-2002; 2002US-0372843P. 17-JUN-2002; 2002US-0389987P. 20-SEP-2002; 2002US-0412418P.

(MITO-) MITOKOR. (BUCK-) BUCK INST AGE RES.

04-APR-2003; 2003WO-US010870

WO2003087768-A2 Homo sapiens.

23-OCT-2003

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This invention relates to novel mitochondrial targets that can be used for therapeutic intervention in treating a disease associated with altered mitochondrial function. Specifically, it refers to a method for identifying proteins of the human heart mitochondrial proteome that are useful for drug screening assays, as well as therapeutic targets. The present invention describes a method for identifying such proteins that can be used in the treatment of various diseases associated with altered mitochondrial function including diabetes mellitus, Huntington's disease, osteoarthritis, Leber's hereditary optic neuropathy (LHON), mitochondrial encephalopathy lactic acidosis and stroke (MELAS), mycolonic epilepsy ragged red fibre syndrome (MERRP) or cancer. Accordingly, these compositions have neuroprotective, nootropic, antidiabetic,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    anticonvulsant, antiarthritic, osteopathic, ophthalmological and cytostatic activities. This polypeptide sequence is a human heart mitochondrial protein of the invention.
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Pred. No. 3.2;
0; Mismatches
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83.3%;
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ABB60410
ID ABB60.
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AC ABB60.
XX
DT 26-MAI
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Gaps ö

ADJ69288 standard; protein; 997 AA.

ADJ69288

RESULT 9
ADJ69288
ID ADJ6
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AC ADJ6
XX

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The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention is useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL16176-ABL30511), expressed DNA ABB72072). The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                            New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signaling and cell-cell
                                        Drosophila; developmental biology; cell signalling; insecticide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; SEQ ID NO 8022; 21pp + Sequence Listing; English.
          Drosophila melanogaster polypeptide SEQ ID NO 8022.
                                                                                                                                                                                                                                                                                                                  Li PWD,
                                                                                                                                                                                                                               23-MAR-2000; 2000US-0191637P.
11-JUL-2000; 2000US-00614150.
                                                                                                                                                                                                23-MAR-2001; 2001WO-US009231
                                                                                                Drosophila melanogaster
                                                                                                                                                                                                                                                                                                                Venter JC, Adams M,
                                                                                                                                                                                                                                                                                                                                                  WPI; 2001-656860/75.
N-PSDB; ABL04513.
                                                                                                                                                                                                                                                                                    (PEKE ) PE CORP NY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 1054 AA;
                                                             pharmaceutical.
                                                                                                                                  WO200171042-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                      interactions.
                                                                                                                                                                27-SEP-2001.
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Myers EW;

Gaps ö Score 65; DB 4; Length 1054; Pred. No. 3.3; 0; Mismatches 2; Indels 84.4%; Best Local Similarity 83.3 Matches 10; Conservative

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ADI28031 standard; protein; 1255 AA. ECMCAD protein 55022490CD1 (first entry) 15-APR-2004 RESULT 11 AD12803

nootropic, antisickling; antianemic; antitumor; anti-HIV; antiallergic; antianemic; antiasthmatic; immunosuppressive; antiatherosclerotic; demaclogical; nephrotrophic; antigout; antithyroid; neuroprotective; osteopathic; antiprophic; antithorit; antithore; antiinflammatory; ophthalmological; anticonvulsant; antiparkinsonian; antibacterial; Virucide; tranquilizer; neuroleptic; antiparkinsonian; cytostatic; hepatotrophic; gene therapy; human extracellular matrix and cell adhesion molecule; ECWCAD; diagnosis; genetic disorder; adrenoleukodystrophy; bown's syndrome; cystic fibrosis; gaucher's disease; myotonic dystrophy; sickle cell anemia; thalassemia; wilms' tumor; immunological disorder; acquired immunodeficiency syndrome;

AIDS; adult respiratory distress syndrome; allergy; anemia; asthma; atherosclerosis; autoimmune hemolytic anemia; contact dermatitis; atherosclerosis; autoimmune hemolytic anemia; contact dermatitis; Goodpasture's syndrome; gout; Grave's disease; multiple sclerosis; soleroporosis; psoriasis; rhumatoid arthritis; scleroderma; systemic lupus erythematosus; ulcerative colitis; uveitis; neurological disorder; epilepsy; stroke; Alzheimer's disease; whitington's disease; Parkinison's disease; multiple sclerosis; huntington's disease; multiple sclerosis; mentalysis; mental disorder; mood; anxiety; meningtis; paget's disease; osteonecrosis; osteomyelitis; chordrosarcomis; dant cell tumor; psoriatic arthritis; chordrosarcomis; systemic sclerosis; cell proliferative disorder; machic keratosis; atherosclerosis; hepatitis; psoriasis; cancer; actinic keratosis; atherosclerosis; hepatitis; psoriasis; cancer; machic keratosis; leukemia; lymphoma; melanoma; myeloma. WO200202634-A2. Homo sapiens. 10-JAN-2002.

29-JUN-2001; 2001WO-US021067. 30-JUN-2000;

2000US-0219462P. 2000US-0240106P. 14-NOV-2000; 2000US-0248887P. 16-NOV-2000; 2000US-0249570P. 2000US-0240111P 2000US-0244021P 18-JUL-2000; 2 12-OCT-2000; 2 12-OCT-2000; 2 27-OCT-2000; 2

(INCY-) INCYTE GENOMICS INC.

Borowsky ML; , Yue H, Azimzai Y, He A, Batra S, Lo TP, Nguyen DB;
JD, Marcus GA, Zingler KA, Gandhi AR, Lal P, Kearney L;
IN, Yao MG, Walia NK, Elliot VS, Patterson C, Khan Fa,
MR, Hafalia AJA, Policky JL, Au-Young J, Lu Y, Borcowsky M
Ramkumar J, Yang J, Guruzajan R, Warren BA, Gietzen K;
Kallick DA, Lee EA, Thangavelu K, Delegeane AM, Lee S; Lu DAM, Ramkumar J, Xu Y, Kallick DA, Burrill JD Burford N, Baughn MR, Tang YT,

WPI; 2002-154732/20. N-PSDB; ADI28067.

Novel isolated human extracellular matrix and cell adhesion molecules useful for treating, preventing connective tissue disorder e.g. osteoporogis, Paget's disease, genetic disorder e.g. cystic fibrosis, thalassemia

Claim 1; SEQ ID NO 23; 270pp; English.

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The invention relates to a novel isolated human extracellular matrix and cell adhesion molecule (referred to as ECMCAD 1-36), its biologically cell adhesion molecule (referred to as ECMCAD 1-36), its biologically cell active or immunogenic fragment or a sequence comprising 90 % identity to ECMCAD 1-36. The molecule is useful for screening a compound for ECMCAD 1-36. The molecule is useful in the diagnosis, treatment and conding nucleic acid are useful in the diagnosis, treatment and correvention of genetic disorder such as adrenoleukodystrophy, Down's prevention of genetic disorder such as adrenoleukodystrophy, bown's cell anemia, thalassemia, Wilms' tumor, etc, immunological disorders such as acquired immunodeficiency syndrome (AIDS), adult respiratory distress syndrome, allergies, anemia, asthma, atherosclerosis, autoimmune cell syndrome, allergies, anemia, asthma, atherosclerosis, autoimmune contact dermatitis, goodpasture's syndrome, gout, emolytic anemia, contact dermatitis, osteoporosis, psoriasis, rheumatoid cravitis, etc., a neurological disorder such as epilepsy, stroke, uveitis, etc., a neurological disorder such as epilepsy, stroke, uveitis, etc., a neurological disorder such as epilepsy, stroke, alsordersis, bacterial and viral meningitis, periodic paralysis, mental disorders including mood, anxiety, and schizophrenic disorders, amnesia, diabetic neuropathy, etc, connective tissue disorder such as disease, osteonecrosis, osteomyelitis, osteomyelitis, osteomyelicis, osteomyelicis, osteomyelicis, architis, systemic sclerosis, etc, and a cell proliferative disorder such as actinic keratosis, atherosclerosis, hepatitis, psoriatis, and actinic keratosis, atherosclerosis, hepatitis, psoriasis, cancers

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                                                                                                                                                                                                                                                angiogenesis; bronchial asthma; Goodpasture's syndrome; metastasis; heart failure; cardiac hypertrophy; chronic ischaemic heart disease; sickle cell disease nephropathy; urinary tract obstruction; haemostatic; skeletal muscle disorder; mycardial infarction; blood vessel disorder; hypertension; atherosclerosis; vasculitis; renal artery stenosis; mumps; gonorrhea; tuberculosis; syphilis; spermatocytic seminoma; osteoporosis; rhabdomyosarcoma; glomerulonephrilis; bone disorder; Paget's disease; rickets; osteomalacia; Hodgkin's disease; gene therapy; antibacterial; cardiant; tumour; thymoma; vasotropic; cytostatic; virucide.
                                                                                                                                                                                                                                        Human; ADAM-TS; A Disintegrin And Metalloproteinase; antiinflammatory;
                                                                      Gaps
including adenocarcinoma, leukemia, lymphoma, melanoma, myeloma, etc.
This sequence represents one of the novel proteins.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note= "Crystallins beta and gamma Greek key motif"
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:e= "Protein kinase C phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            note= "Casein kinase II phosphorylation site"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     313. .315 _ _ ____/notes ... /notes "Protein kinase C phosphorylation site" 342. .345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 note= "Protein kinase C phosphorylation site"
                                                 DB 5; Length 1255; 3.9;
                                                                                                                                                                                                                                                                                                                                                                                                                     31. .1686
/label= Human_mature_27875_ADAM-TS_protein
                                                                                                                                                                                                                    Human 27875 ADAM-TS (a disintegrin and metalloproteinase).
                                                                     2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Casein kinase II phosphorylation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Protein kinase C phosphorylation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Cell attachment sequence"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            'label= Metalloproteinase_domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                   "N-myristoylation site"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        note= "N-myristoylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note= "N-glycosylation site"
110. .112
                                                Score 65; DB 5
Pred. No. 3.9;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                 1. .30
/label= Signal_peptide
                                                                                                                                                         AAE00934 standard; protein; 1686 AA.
                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
                                                            83.3%;
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/note= "Ce
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                                                                                                    113 WSAWSICSRSCG 124
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                                                                    10; Conservative
                                                                                      1 WSGWSSCSRSCG 12
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                                                Query Match
Best Local Similarity
                             Sequence 1255 AA;
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                                                                                                                                                                              AAE00934;
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                                                                                                                                       RESULT 12
AAE00934
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note= "Growth factor and cytokine metalloproteinase
amily signature 2 domain"
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                                                                                                                                                           "Casein kinase II phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .571
3= "Protein kinase C phosphorylation site"
                               "Protein kinase C phosphorylation site"
                                                              "Casein kinase II phosphorylation site"
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"Casein kinase II phosphorylation site"
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                                                                                             "N-myristoylation site"
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74. .779
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  542. .592
/label= Thrombospondin_domain
                                                                                                                                                                                                                                                         'label= Thrombospondin_domain
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/label= Thrombospondin_domain
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                                                                                                           185. .394
/label= Zinc_binding_domain
                                                                                                                                                                                                                                                                                                                                                                                                                       341. .592
/label= Disintegrin_domain
                                                                                                                                                                                          "Amidation site"
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/note= "N
98
                                                                                                                                         .404
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765. .770
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716. .721
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Gaps

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Query Match Best Local Similarity

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angiogenesis; bronchial asthams, Goodpasture's syndrome; metastasis; heart failure; cardiac hypertrophy; chronic ischaemic heart disease; sickle cell disease nephropathy; urinary tract obstruction; haemostatic; sickle cell disease nephropathy; urinary tract obstruction; haemostatic; skeletal muscle disorder; myocardial infarction; blood vessel disorder; hypertension; atherosclerosis; vasculitis; renal artery stenosis; mumps; phonortheas; tuberculosis; syphilis; spermatocytic seminoms; osteoporosis; rhabdomyosarcoma; glomerulonephritis; bone disorder; Paget's disease; rickets; osteomalacia; Hodgkin's disease; gene therapy; antibacterial; cardiant; tumour; thymoma; vasotropic; cytostatic; virucide.
                                                                                                                                                                                                                                                                                                                                                                                                                  Human; ADAM-TS; A Disintegrin And Metalloproteinase; antiinflammatory;
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.e= "Crystallins beta and gamma Greek key motif"
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379. .384
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Mote= "Protein kinase C phosphorylation site"
442. .345
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e= "Protein kinase C phosphorylation site"
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| Jabel= Human_mature_27875_ADAM-TS_protein
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label= Metalloproteinase_domain
                                                                                                                                                                                                                                                                                                                                                                      Human 27875 ADAM-TS protein, alternative version.
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       Mismatches
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|abel= Signal_peptide
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                                                                                                                                                                                                                             AAE00913 standard; protein; 1686 AA.
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/note= ""
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                                                                                                       544 WSAWSICSRSCG 555
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          Conservative
                                                      1 WSGWSSCSRSCG 12
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            Matches
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83.3%;
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1592. .1597
//note= "W-myristoylation site"
1599. .1601
/note= "Protein kinase C phosphorylation site"
1606. .1609
/note= "CAMP- and CGMP-dependent protein kinase
phosphorylation site"
                                              /note= "N-glycosylation site"
1005. .1010
/note= "N-myristoylation site"
1006. .1009
1001. .1014
/note= "Casein kinase II phosphorylation site"
                                                                                                                                                                                          1039. .1044
/note= "N-myristoylation site"
/note= "Casein kinase II phosphorylation site"
1263. .1268
1264. .1266
/note= "N-myristoylation site"
/note= "N-myristoylation site"
                                                                                                                                                                                                                                                                                                                           308. .1311 note= "Casein kinase II phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1419. .1422
/note= "N-glycosylation site"
1440. .1443
1400. .1442
/note= "Protein kinase I phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 fig. 1522

Inote= "N-myristoylation site"

Inote= "Casein kinase II phosphorylation site"

Inote= "protein kinase C phosphorylation site"

Inote= "protein kinase C phosphorylation site"

Inote= "Casein kinase II phosphorylation site"
                                                                                                                                                                035. 1037
note= "Protein kinase C phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                         358. 1363
hote= "N-myristoylation site"
7070. 1370. 1371
hote= "Protein kinase C phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                       385. 1387
note= "Protein kinase C phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                        397. .1400
note= "Casein kinase II phosphorylation site"
412. .1415
          'note= "Protein kinase C phosphorylation site"
171. .974
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 4; Length 1686;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    note= "N-glycosylation site"
415. .1463
label= Thrombospondin_domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .466. .1521
|abel= Thrombospondin_domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
84.4%; Score 65; DB
Best Local Similarity 83.3%; Pred. No. 5;
Matches 10; Conservative 0; Mismatches
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                                                                                                                                                                                                                                         note= "Growth factor and cytokine metalloproteinase amily signature 2 domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 note= "cAMP- and cGMP-dependent protein kinase hosphorylation site"
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/note= "N-glycosylation site"
957. .960
/note= "Casein kinase II phosphorylation site"
                                              "Casein kinase II phosphorylation site"
                                                                                                                                                                        "Casein kinase II phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                    'note= "Protein kinase C phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tabel= Unknown
fnote= "Encoded by CRC"
598. .600
note= "Protein kinase C phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Casein kinase II phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           note= "Casein kinase II phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Cytochrome C family heme-binding site"
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65. .770
                                                                                                              "N-myristoylation site"
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note= "N-myristoylation site"
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                                                                                                                                            Thrombospondin_domain
                                                                                                                                                                                                                                                                                                                                                       Thrombospondin domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          25. .868
label= Thrombospondin_domain
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label= Thrombospondin_domain
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385. .394
/label= Zinc_binding_domain
                                                                                                                                                                                                                                                                                                       41. .592
|abel= Disintegrin_domain
                                                                            "Amidation site"
                                                                                                                                                                                                                                                                                                                              . .619
.note= "N
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.note= "C
38.
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,note= ".
,696
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'note= ""
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Gaps

AAB74944;

RESULT 14 AAB7494 16-JAN-2001.

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The present invention relates to an isolated 27875, 22025, 27420, 17906, 16319, 55092, or 10218 nucleic acid molecule. The invention is useful for diagnosing or treating cancer or aberrant cellular proliferation and/or differentiation, immune disorders, heart disorders, cardiovascular disorders including endothelial cell disorders, haematopoietic disorders, blood vessel disorders, brain disorders, pain and metabolic disorders, liver disorders and platelet disorders. The invention is also useful in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New isolated 27875, 22025, 27420, 17906, 16319, 55092, or 10218 nucleic acid molecules, useful for diagnosing or treating cancer, pain, or immune, endothelial cell, hematopoietic, blood vessel, brain, metabolic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 gene therapy. The present sequence is human ADAM-TS protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 1686;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Macbeth KJ,
"Human mature ADAM-TS protein"
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                              'note = Metalloproteinase domain
                                                                                                              542. .592
/note = S thrombospondin domain
                                                                                                                                                                                825. .868
/note = S thrombospondin domain
949. .988
/note = S thrombospondin domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 8;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  84.4%; Score 65; DB
ilarity 83.3%; Pred. No. 5;
Conservative 0; Mismatches
                                                              Zinc-binding domain
                                                                                                /note = Disintegrin domain
                                                                                                                                                                                                                                                                           1466. .1521
/note = S thrombospondin
                                                                                                                                                                                                                                                            note = S thrombospondin
                                                                                                                                                                                                                                                                                                                         'note= "Encoded by GAC"
                                                                                                                                                                                                                                                                                                                                                         'note= "Encoded by CAT"
                                                                                                                                                               'note= "Encoded by CRC"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10.ARR-2000; 2000US-0254037P.
10.ARR-2001; 2001US-00833082.
16-MAY-2001; 2001US-00860193.
31-OCT-2001; 2001US-01360193.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (MILL-) MILLENNIUM PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        11-MAR-2003; 2003US-00386414.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     99US-00426282
2000US-00571689
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      99US-00330970
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  29-OCT-2002; 2002US-00283023
                                                                                                                                                                                                                                              1415. .1463
                .259
                                                      .394
                                                                                    . 592
                                                                     note =
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Kapeller-Libermann R,
Cook WJ, Meyers RE,
                                                                                                                                                                                                                                                                                                             1479
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 and liver disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2004-081738/08
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nes 10; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 1686 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 N-PSDB; ADJ58901
                                                                                                                                                                                                                                                                                                               Misc-difference
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                                                                                                                                                                                                                                                                                                                                               Misc-difference
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        16-MAY-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           22-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        11-JUN-1999;
25-OCT-1999;
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Matches
                                                                                                                                                                                   Domain
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present sequence represents a disintegrin and metalloprotease (ADAM) type metal protease designated MDTS1, isolated from human. MDTS proteins have cytostatic and antiarthritic activities. They can be used as a drug for cancers, arthritis and arthrosis deformans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               27875; 22025; 27420; 17906; 16319; 55092; 10218; cancer; cellular proliferation; cellular differentiation; immune disorder; cardidvescular disorder; endothelial cell disorder; hacenatopoietic disorder; blood vessel disorder; brain disorder; pain; matabolic disorder; liver disorder; platelet disorder; gene therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                  Human; a disintegrin and metalloprotease type metal protease; MDTS1;
MDTS2; MDTS3; ADAM type metal protease; cytostatic; antiarthritic;
cancer; arthritis; arthrosis deformans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New metal protease and metal protease gene, for use as a drug for cancers, arthritis and arthrosis deformans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 65; DB 4; Length 1686;
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                                                                                                                                       Human ADAM type metal protease MDTS1 protein SEQ ID NO:1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pred. No. 5;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1. .30
/label= Signal_peptide
31. .1686
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 1; Page 12-17; 31pp; Japanese.
                                               AAB74944 standard; protein; 1686 AA
                                                                                                                                                                                                                                                                                                                                                                                                   (YAMA ) YAMANOUCHI PHARM CO LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human ADAM-TS protein, 27875.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               84.4%;
83.3%;
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                                                                                                              (first entry)
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human; ADAM-TS; enzyme.
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                                                                                                               02-JUL-2001
                                                                                                                                                                                                                                              Ношо варіеля
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Carroll JM;

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Peptide

Protein

ADJ58902;

Query Match

Matches

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Search completed: April 1, 2005, 13:54:26 Job time: 85.7391 secs

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OM protein - protein search, using sw model

April 1, 2005, 13:24:31; Search time 75.6522 Seconds (without alignments) 81.226 Million cell updates/sec Run on:

US-09-462-909D-7 62 1 WSXWSXCSXXCG 12 Title: Perfect score: Sequence: BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

1612378 seqs, 512079187 residues Searched:

1612378 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

UniProt_03:*
1: uniprot_Sprot:*
2: uniprot_trembl:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		•			SUMMARIES	÷
Result		Query				
No.	Score	Match	Match Length	BB	QI	Description
-4	28	93.5	504	7	Ф69НГ7	
N	.58	93.5	3869	N	Q86PQ3	Q86pq3 cryptospori
m	57	91.9	238.	N	076510	
4	57	91.9	257	7	Q966K7	
S	57	91.9	872	~	Q22580	
9	57	91.9	1077	-	SMSA MOUSE	
7	57	91.9		~	Q7QC32	Q7qc32 anopheles g
Φ.	57	91.9			Q8CG65 .	ın
σ,	57	91.9	5141		Q700K0	Q700k0 rattus norv
10	26	90.3		N	043982	043982 cryptospori
11	26	90.3	156	~	QBMXY6	Q8mxy6 cryptospori
12	26	90.3	168	7	Q9GZ21	Q9gz21 cryptospori
13	26	90.3	168	N	Q9GZ22	_
14	26	90.3	168	~	Q9GZ23	~
15	26	90.3	192	~	Q7JN23	_
16	26	90.3	449	7	Q8QFV1	_
17	26	90.3	461	7	095522	
18	26	90.3	549	~	Q8T988	
19	26	90.3	612	~	96 0 Z9 0	Q6zq96 mus musculu
20	26	90.3	628	7	Q7KRF4	Q7krf4 drosophila
21	26	90.3	654	7	Q19284	Q19284 caenorhabdi
22	26	90.3	959	~	Оверов	Q86pq8 cryptospori
23	26	90.3	099	~	Q23832	Q23832 cryptospori
24	26	90.3	687	7	023729	
22	26	90.3	724	7	004588	
26	26	90.3	763	~	O0XXDO	
27	26	ö	839	7	Q8ML26	Q8m126 drosophila
28	26	90.3	867	Н	SSPO_BOVIN	P98167 bos taurus
29	26	ö	880	~	Q8MSF8	Q8msf8 drosophila
30	99	90.3	880	~	Q9VKV3	drosc
31	26	90.3	997	H	ATS7_HUMAN	Q9ukp4 homo sapien

Q9u631 drosophila Q8t3a0 ciona intes Q7yu67 drosophila Q9ytt0 drosophila Q6ytt0 drosophila Q6pd18 mus musculu Q6pd18 mus musculu Q8mya8 caenorhabdi O60242 homo sapien Q802f8 mus musculu Q69aug mus musculu Q69aug mus musculu Q69aug mus musculu	
Q9U631 Q8T3A0 Q7YU67 Q9YTT0 Q8PL1 Q6PD18 BAI3 HUMAN BAI3 HUMAN BAI3 MOUSE Q6SSA9 Q6SSA9	Q9XTP6 Q25757
000000011000	0 0
1081 1089 1089 1282 1361 1522 1522 1641 1668	1905 2098
	90.3 90.3
	56 56
0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	4 4 3.

ALIGNMENTS

477 WSAWSACSTSCG 488 1 WSXWSXCSXXCG 12 ઠે g

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RESULT 2 Q86PQ3 ID Q86PQ3

PRT; 3869 AA. PRELIMINARY;

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WormBase; WBGene00017471; F14H12.3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
STRAIN=Bristol N2;
Nelson J., Gattung S., R Wilson.;
                                                                                                                                                                                                            Query Match 91.9
Best Local Similarity 66.7
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                     1 WSXWSXCSXXCG 12
                                                                                                                                                                                                                                                                                                                                                  47 WSSWSACSKSCG 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (NOV-2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A. STRAIN-Bristol N2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A. STRAIN=Bristol N2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN-Bristol N2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A. STRAIN=Bristol N2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN-Bristol N2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Waterston R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Waterston R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q966K7
                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 4
Q966K7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STIRBBR
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                                                                                                                                                                                                                             SEQUENCE FROM N.A.
MEDLINE=22326344; PubMed=12438378;
DOI=10.1128/IAI.70.12.6987-6995.2002;
Deng M., Tabjeton T.J., London N.R., Bauer C., Schroeder A.A.,
Abrahamsen M.S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                          Cryptosporidium parvum genes containing thrombospondin type 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 58; DB 2; Length 3869;
Pred. No. 2.4;
0; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
STRAIN=Moredun;
Spano F., Putignani L., Crisanti A.;
Submitted (JUN-1998) to the EMBL/GenBank/DDBJ databases.
EMBL, AR079818; AAC26612.1;
HSSP, P07996; ILSL.
InterPro; IPR002086; Aldehyd_dehydrog.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         25 Potential.
429514 MW; 1F4851B7B0787B87 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cryptosporidium parvum.
Bukaryota, Alveolata; Apicomplexa; Coccidia; Bimeriida; Cryptosporidiidae; Cryptosporidium.
                                                                                            TSPI domain-containing protein TSP2 precursor.
Cryptosporidium parvum.
Bukaryota; Alveolata; Apicomplexa; Coccidia; Bimeriida;
Cryptosporidiidae; Cryptosporidium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-NOV-1998 (TrEMBLrel. 08, Created)
01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-NAN-2004 (TrEMBLrel. 26, Last annotation update)
Thrombospondin-related adhesive protein (Fragment).
                           01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROSITE; PS00109; 4FF4S FERREDOXIN; UNKNOWN 3. PROSITE; PS00070; ALDEHYDE DEHYDR_CYS; UNKNOWN_1 PROSITE; PS50092; TSP1; 10.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               238 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GO; GO:0016020; C:membrane; IEA.
GO; GO:0030154; P:cell differentiation; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR001450; 4Fe48_Enredoxin.
InterPro; IPR0012086; Aldehyd dehydrog.
InterPro; IPR001808; Aldehyd dehydrog.
InterPro; IPR001808; ShKT.
InterPro; IPR001808; Sushi, SCR_CCP.
InterPro; IPR001808; Sushi, SCR_CCP.
InterPro; IPR0018084; TSP1.
InterPro; IPR0018084; TSP1.
InterPro; IPR0018084; INTERPO; IPR0180894; INTERPO; IPR0180994; INTERPO; IPR0180994; INTERPO; INTE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                                                                                                      Infect. Immun. 70:6987-6995(2002).
EMBL; AX190984; AA039046.1; -.
HSSP; P07996; 1LSL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 93.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 66.7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               386 WSSWSSCSTSCG 397
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 WSXWSXCSXXCG 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6
3869 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                          domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    076510
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076510
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01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 24, Last annotation update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Hypothetical protein F14H12.3.
Name=F14H12.3; ORFNames=F14H12.3;
Caenorhabditis elegans.
Caenorhabditis elegans.
Rhabditidae, Peloderinae; Caenorhabditis.
NGBLTATOLES PELOGERINAE; Caenorhabditis.
NGBLTAXID=6239;
                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=99060513; PubMed=9851916; MormBese Consortium; hormase Consortium; Generated C. elegans: a platform for "Genome sequence of the nematode C. elegans Sequencing Consortium."; investigating biology. The C. elegans Sequencing Consortium."; Science 282:2012-2018(1998).
                                                                                                                                                                                                                                                                                                                                                            0
                                                                                                                                                                                                                                                                                         91.9%; Score 57; DB 2; Length 238; 66.7%; Pred. No. 0.35; ive 0; Mismatcheg 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WormBase Consortium;
Submitted (SEP-2004) to the EMBL/GenBank/DDBJ databases.
RMBL; AC006630; AAK68325.1; -.
HSSP; P07996; 1LSL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "The sequence of C. elegans cosmid F14H12.";
Submitted (MAR-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Waterston R.H.;
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Waterston R.;
Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                238 AA; 26307 MW; 28242DE88F62C5A2 CRC64;
InterPro; IPR000984; TSP1.
PEam; PF00090; TSP 1; 3.
SMART; SM00090; TSP1; 3.
PROSITE; PS50092; TSP1; 3.
PROSITE; PS50092; TSP1; 3.
NON_TER 1 1
NON_TER 28 28
SEQÜENCE 238 AA; 26307 MW; 28242DE88F62C55A2 Ci
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        257 AA
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872 AA; 98040 MW; 1BA1D480AEF0ED15 CRC64;
    SEQUENCE
                                                                                                                                                                                                                                                SM5A MOUSE
                                                                                                                                                                셤
                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Genome sequence of the nematode C. elegans: a platform for investigating biology. The C. elegans Sequencing Consortium."; Science 282:2012-2018(1998).
                                                                                                                                                                                                   Score 57; DB 2; Length 257; Pred. No. 0.37; 0; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HSSP; P07956; 1LSL.

WormBase; WBGene00020567; T19D2.1.

WormBase; WBGene00020567; T19D2.1.

WormBase; WBGene00020567; T19D2.1.

WormBase; WBGene00020567; T19D2.1.

GO; GO:0005508; P:proteolysis and peptidolysis; IEA.

InterPro; IPR001059; Peptidase M.2B.

InterPro; IPR001059; Pept M.Zn_BS.

InterPro; IPR0010519; Pept M.Zn_BS.

InterPro; IPR000684; TSP1.

Pfam; PP01041; Reprolysin; 1.

Pfam; PP01090; TSP 1; 4.

SMART; SM00209; TSP 1; 4.

SMART; SM00209; TSP1; 4.

PROSITE; PS50015; ADAM MEPRO; 1.

PROSITE; PS500142; ZNIC_PROTEASE; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WormBase Consortium;
Submitted (SRP-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; 142246; AAA83600.2; -.
PIR; T16892; T16892.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "The sequence of C. elegans cosmid T19D2.";
Submitted (JAN-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Waterston R.; Submitted (NOV-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                   PROSITE; PS50092; TSP1; 3.
Hypothetical protein.
SEQUENCE 257 AA; 26512 MW; 9B052A0D07F2BEFF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-NOV-1996 (TrEMBLrel. 01, Created)
01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                    872 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=Bristol N2;
MEDLINE=99069613; PubMed=9851916;
WormBase Consortium;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hypothetical protein T19D2.1.
Name=T19D2.1; ORFNames=T19D2.1;
                                                                                                                                                                                                     91.9%;
                                                       Pfam; PP00090; TSP 1; 3.—
PRINTS; PR01705; TSP1REPEAT.
SMART; SM00209; TSP1; 3.
                 InterPro, IPR000884; TSP1.
InterPro, IPR008085; TSP 1.
  WormPep; F14H12.3; CE07063
                                                                                                                                                                                                                                                                                                                             145 WSSWSACSVTCG 156
                                                                                                                                                                                                                          Local Similarity 66.7
Les 8; Conservative
                                                                                                                                                                                                                                                                                      1 WSXWSXCSXXCG 12
                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Caenorhabditis elegans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A. STRAIN=Bristol N2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN-Bristol N2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE PROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN-Bristol N2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=6239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bentley D.;
                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                    022580
                                                                                                                                                                                                                                                                                                                                                                                         RESULT 5
022580
101-M
DT 01-M
DE NAMED
OX CASEN
COX NCBI
RN SEQU
RX STRA
RX MEDL
RY SEQU
RY STRA
RY BEDL
RY SEQU
RY STRA
RY WATH
DR SUMM
DR WOTH
DR EMBI
DR EMBI
DR EMBI
DR FEMI
DR FORE
DR INTE
DR HOSSI
DR PROS
DR PROS
DR PROS
ENDR PROS
DR PROS
ENDR
DR PROS
DR PROS
ENDR PROS
E
SKRRRRRR
                                                                                                                                                                                                                                                                                      8
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                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Developmental protein; Glycoprotein; Multigene family; Neurogenesis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -1- DEVELOPMENTAL STAGE: Differentially expressed in embryonic and adult tissues. Its abundance decreases from E10 to birth.
-1- SIMILARITY: Balongs to the semaphorin family.
-1- SIMILARITY: Contains 1 Sema domain.
-1- SIMILARITY: Contains 7 TSP type-1 domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                         ö
     Length 872;
                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MGD; MGI:107556; Sema5a.
GO: GO:0016021; C:integral to membrane; IDA.
GO: GO:000846; F:axon guidance receptor activity; IDA.
GO: GO:0007411; P:axon guidance; IMP.
                                                                                                                                                                                                                                                                                                  SMSA_MOUSE STANDARD; PRT; 1077 AA. 062217; 30-MAY-2000 (Rel. 39, Created) 30-MAY-2000 (Rel. 39, Last sequence update) 25-OCT-2004 (Rel. 45, Last annotation update) 25-OCT-2004 (Rel. 45, Last annotation update) Name-Semasa; Synonyms-Semaf, Sem?; House) Muse usculus (Mouse)
  Score 57; DB 2;
Pred. No. 1;
                                                         0: Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR003659; Plexin-like.
InterPro; IPR002165; Plexin_repeat.
InterPro; IPR001627; Sema.
InterPro; IPR00884; TSP1.
InterPro; IPR008885; TSP_1.
Pfam; PF01437; PSI.
Pfam; PF01403; Sema; 1.
Pfam; PF00090; TSP_1; 5.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pfam; PF00090; TSP_1; 5.
PRINTS; PROLITOS; TSPIREPEAT.
SWART; SW00423; PSI; 1.
SWART; SW00620; Sema; 1.
SWART; SW00209; TSPI; 6.
PROSITE; PSS1004; SEMA; 1.
PROSITE; PSS0092; TSPI; 6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; X97817; CAA66397.1; -. HSSP; P07996; 1LSL.
Query Match 91.9%;
Best Local Similarity 66.7%;
Matches 8; Conservative
                                                                                                                                                                831 WSSWSSCSTKCG 842
                                                                                                             1 WSXWSXCSXXCG 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
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PF05375;
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Q8CG65;
01-MAR-2003 (
NON TER
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SEQUENCE
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PRINTS;
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                                                                                                                   Q8CG65
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                                                                                                                                                                                                                                                                                                                                                                                    Name=ebiG1179; ORFNames=ENSANGG0000001015;
Anopheles gambiae str. PEST:
Bukaryota; Metazoa; Arthropoda; Hèxapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Anopheles.
NCBI_TaxID=180454;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Anopheles Genome Sequencing Consortium;
Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
-!- CAUTION: The sequence shown here is derived from an
EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
                                                                                                                                                                                                            (Potential). (Potential). (Potential).
                                                                                                                                                                                    (Potential)
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                                                                                                                                                                                                     (Potential)
                                                                                                                                                                                                                                                    Score 57; DB 1; Length 1077; Pred. No. 1.2; 0; Mismatches 4; Indels
                                                                                                                                                                                                                                     120826 MW; EDABODDDA42789FF CRC64;
           Semaphorin 5A.
Extracellular (Potential).
Potential.
                                  Cytoplasmic (Potential)
                                                                                                                                                                                                                                                                                                                                                        Q7QC32;
U-MAR-2004 (TrEMBLrel. 26, Created)
01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
                                                                                                                                                                                                              (GlcNAc.
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(GlcNAc.
                                                                                                                                                                                      N-linked (GlcNAc
N-linked (GlcNAc
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GO; GO:0004872; F:receptor activity; IEA.
InterPro; IPR001165; Plexin_repeat.
InterPro; IPR001637; Sema.
InterPro; IPR001884; TSP1.
InterPro; IPR008884; TSP1.
Pfam; PF01403; Sema; 1.
Pfam; PF01403; Sema; 1.
Pfam; PF01403; Sema; 1.
Pfam; PF01403; TSP1; 5.
PRINTS; PR01705; TSP1RPEAT.
                                                                                                                                                                                                                                                                                                                                                PRT; 1093 AA.
                                                                   TSP type-1 3.
TSP type-1 4.
TSP type-1 5.
TSP type-1 6.
TSP type-1 7.
By similarity.
   Potential
                                                                                                                                                                              N-linked
                                                                                                                                                                                                                      linked
                                                                                                                                                                                                                              N-linked
                                                                                                                                                                      N-linked
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                                                                                                                                                                                                                                                       91.9%;
66.7%;
                                                                                                                                                                                                                                               Query Match
Best Local Similarity 66...
Second Similarity 66...
Second Similarity 66...
                                                                                                                                                                                                                                                                                                       847 WSSWSKCSATCG 858
                                                                                                                                                                                                                                                                                       1 WSXWSXCSXXCG 12
                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
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                                                                                                                                                                                                                              933 93
1077 AA;
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DISULFID
DISULFID
CARBOHYD
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CARBOHYD
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CARBOHYD
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                    DOMAIN
TRANSMEM
DOMAIN
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STRAIN=ICR; TISSUE-Brain;
STRAIN=ICR; TISSUE-Brain;
Goncalves N., Simon-Chazottes D., Creveaux I., Meiniel A.,
Guenet J-L., Meiniel R.;
"Mouse SCO-spondin, a gene of the thrombospondin type 1 repeat (TSR)
superfamily expressed in the brain.";
Gene 312:263-270(2003).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mus musculus (Mouse).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                            ö
                                                                                           Length 1093;
1
1093 1093
1093 AA; 118842 MW; 2DB86BEC7CB42230 CRC64;
                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                      Ol-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
SCO-spondin.
Name-Scoospondin; Synonyms=sco-spondin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PROSITE; PS00196; COPPER BLUB; UNKNOWN_1.
PROSITE; PS01125; CTCK_2; 1.
PROSITE; PS01186; EGF_2; 2.
PROSITE; PS50022; PS6G_3; 1.
PROSITE; PS00261; GLYCO_HORMONE_BETA_1; UNKNOWN_2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -!- SIMILARITY: Contains 1 F5/8 type C domain.
EMBL; AJ491857; CAD42654.1; -.
HSSP; PO1130; AD4.0.
MGI: A574311; Scospondin.
GO; GO:0005737; C:Cytoplasm; IC.
InterPro; IPR000923; Blucku.!.
InterPro; IPR000923; Blucku.!.
InterPro; IPR005207; Cygrich TIL.
InterPro; IPR005207; Cygrich TIL.
InterPro; IPR005207; Cygrich TIL.
InterPro; IPR065209; EMP.
                                                                                             Score 57; DB 2;
Pred. No. 1.2;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                         PRT; 4998 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR011489; EMI.
InterPro; IPR0016421; FA58 C.
InterPro; IPR001545; G1y.hormoneB.
InterPro; IPR00172; LDL receptor
InterPro; IPR008037; Prot_inh_PWP_
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              F5 F8 type C; 1.
LdI recept a; 10.
Pacifastin I; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PF00094; VWD; 2.
S; PR00261; LDLRECEPTOR.
S; PR01705; TSP1REPEAT.
                                                                                                  91.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              nterPro; IPR008085; TSP_1.
nterPro; IPR001007; VWF_C.
nterPro; IPR001846; VWF_D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       fam; PF01826; TIL; 10.
fam; PF00090; TSP 1; 25.
fam; PF00093; VWC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LDLa; 10.
TSP1; 25.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SMART; SM00231; FA58C; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      interPro; IPR000884; TSP1
                                                                                        Query Match
Best Local Similarity 66.7
Marches 8; Conservative
                                                                                                                                                                                                                                                  586 WSAWSACSQTCG 597
                                                                                                                                                                                                   1 WSXWSXCSXXCG 12
                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
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SMART; SM00209; TSP1; 2
SMART; SM00214; VWC; 4.
SMART; SM00216; VWD; 2.
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Gaps

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SEQUENCE FROM N.A.
STRAIN=P12;
MEDLINE=98443215; PubMed=9769250; DOI=10.1006/expr.1998.4324;
MEDLINE=98443215; PubMed=9769250; DOI=10.1006/expr.1998.4324;
Spano F., Putignani L., Guida S., Crieanti A.;
"Cryptosporidium parvum: PCR-RFLP analysis of the TRAP-C1 (thrombosporodin.related adhesive protein of Cryptosporidium-1) gene discriminates between two alleles differentially associated with parasite isolates of animal and human origin.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 56; DB 2; Length 106;
Pred. No. 0.26;
0; Mismatches 4; Indels
                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Satch M., Kimata I., Iseki M., Nakai Y.;
Submitted (AUG-2002) to the EMBL/GenBank/DDBJ databases.
BMBL; AB089293; BAC07243.1; -.
HSSP; P07996; 1LSL.
InterPro; IPR000884; TSP1.
Pfam; PF00090; TSP1; 1.
SMART; SM00209; TSP1; 2.
PROSITE; PS50092; TSP1; 2.
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Cryptosporidiidae, Cryptosporidium.
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Cryptosporidiidae, Cryptosporidium.
NCBI_TaxID=5807;
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                                                                                                                                                                                                                                                                                                                                                                                    Last sequence update)
Last annotation update)
                                         4;
                                                                                                                                                                                                                                                                                                106 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        156 AA.
           Pred. No. 4.3;
                                         0; Mismatches
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01-OCT-2002 (TrEMBLrel. 22, Last seq
                                                                                                                                                                                                                                                                                                                                                         Created)
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                                                                                                                                                                                                                                                                                                PRT;
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EMBL; AF033828; AAB92609.1; -
     66.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 66.7%;
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                        043982;
01-JUN-1998 (TrEMBLrel. 06,
01-JUN-1998 (TrEMBLrel. 06,
01-MAR-2003 (TrEMBLrel. 23,
                                                                                                                                            4161 WSAWSACSHSCG 4172
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Pfam; PF00090; TSP 1; 1.
SMART; SM00209; TSP1; 2.
PROSITE; PS50092; TSP1; 2.
                                   8; Conservative
                                                                                            1 WSXWSXCSXXCG 12
                                                                                                                                                                                                                                                                                             PRELIMINARY;
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     Best Local Similarity
Matches 8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Name=TRAP-C1
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NON TER
SEQUENCE
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                                                                                                                                                                                                                                     RESULT 10
043982
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Rattus norvegicus (Rat).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Meiniel O.;
Submitted (MAR-2004) to the EMBL/GenBank/DDBJ databases.

- 1- SIMILARITY: Contains 1 F5/8 type C domain.

R KMEL; AJ629845; CAFF33425.1; -.

R HSSP; P01130; 1AJJ.

R GO, GO:0007155; P:cell adhesion; IEA.

R InterPro; IPR002919; Cysrich TIL.

R InterPro; IPR002019; Cysrich TIL.

R InterPro; IPR002019; EMF_C.

R InterPro; IPR001489; EMI.

R InterPro; IPR001489; EMI.

R InterPro; IPR001489; EMI.

R InterPro; IPR001489; EMI.

R InterPro; IPR001649; EMI.

R InterPro; IPR001649; TSPI.

DR InterPro; IPR001684; TSPI.

DR InterPro; IPR001089; TWC_Out.

DR InterPro; IPR001007; VWF_C.
                                                                                                                                                                                                    91.9%; Score 57; DB 2; Length 4998;
66.7%; Pred. No. 4.2;
ive 0; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             91.9%; Score 57; DB 2; Length 5141;
PS01209; LDLRA_1; 8.
PS50068; LDLRA_2; 10.
PS50092; TSP1; 25.
PS01208; WMFC_1; UNKNOWN_1.
PS50184; VWFC_2; 2.
4998 AA; 535028 MW; DA2ABABDA47DF225 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
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PROSITE; PS01186; EGF 2; UNIXNOWN 2.
PROSITE; PS50022; PS5G 3; UNIXNOWN 2.
PROSITE; PS00261; GLYCC_HORMONE_BETA_1; UNKNOWN_2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT; 5141 AA
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Pfam; PR0754; F5 F8_type_C; 1.
Pfam; PF00057; LdI_recept_a; 8.
Pfam; PF01826; T1L; 10.
Pfam; PR00099; TSP_1; 25.
Pfam; PR00094; VWC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRINTS; PRO0261; LDLRECEPTOR.
SWART; SM00192; LDLa; 10.
SWART; SM00219; TSP1; 25.
SWART; SM00214; VWC; 5.
SWART; SM00215; VWC out; 9.
                                                                                                                                                                                                                                                                                                                                                                              4012 WSAWSSCSHSCG 4023
                                                                                                                                                                                                                               Local Similarity 66.7
les 8; Conservative
                                                                                                                                                                                                                                                                                                                     1 WSXWSXCSXXCG 12
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MEDILINE=COSB8602; PubMed=10930736;
MEDILINE=COSB8602; Amar C., McLauchlin J.;
Pedraza-Diaz S., Amar C., McLauchlin J.;
"The identification and characterisation of an unusual genotype of cryptosporidium from human faeces as Cryptosporidium meleagridis.";
FEMS Microbiol. Lett. 189-194 (2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
MEDLINE=20189602; PubMed=10930736;
MEDLINE=20189602. Amar C., McLauchlin J.;
Pedraza-Diaz S., Amar C., McLauchlin J.;
"The identification and characterisation of an unusual genotype of cryptosporidium from human faeces as Cryptosporidium meleagridis.";
PEMS Microbiol. Lett. 189:189-194 (2000).
HSSP; P07996; 1LSL.
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Pred. No. 0.37;
0; Mismatches 4; Indels
                                                                                     Query Match 90.3%; Score 56; DB 2; Length 156; Best Local Similarity 66.7%; Pred. No. 0.35; Matches 8; Conservative 0; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Cryptosporidium parvum.

Bukaryota, Alveolata; Apicomplexa; Coccidia; Bimeriida;

Cryptosporidiidae; Cryptosporidium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bukaryota, Alveolata, Apicomplexa, Coccidia, Bimeriida,
Cryptosporidiidae, Cryptosporidium.
NCBI_TaxID=91969;
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             1 1
156 156 156 17312 MW; 6439FF81F221047E CRC64;
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01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Thrombospondin-related adhesive protein (Fragment).
                                                                                                                                                                                                                                                                                                                                                                            01-WAR-2001 (TrEMBLrel. 16, Created)
01-WAR-2001 (TrEMBLrel. 16, Last sequence update)
01-WAR-2004 (TrEMBLrel. 26, Last annotation update)
Thrombospondin-related adhesive protein (Fragment).
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Best Local Similarity 66.7%;
Matches 8; Conservative (
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Pfam; PF00090; TSP1; 2.
SMART; SM00209; TSP1; 3.
PROSITE; PSS0092; TSP1; 3.
NON TER 16 168
SEQUENCE 168 AA; 18576 MM
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SEQUENCE
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MEDINE_CORRECTIONS OF THE MEDINE_CORRECTIONS OF THE Identification and characterisation of an unusual genotype of The identification and characterisation of an unusual genotype of Cryptosporidium from human faeces as Cryptosporidium meleagridis."; FEMS Microbiol. Lett. 189:189-194(2000).

FEMS. PROTOSPS, 1LSL.
InterPro; INFOURBH; TSP1.
FEMS.; PROTOSPS, 1LSP.
InterPro; INFOURBH; TSP1.
FEMS.; PROTOSPS, TSP1; 3.
PROSITE; PS50092; TSP1; 3.
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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
TRAP-C1 (Thrombospondin related adhesive protein) (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ouery Match 90.3%; Score 56; DB 2; Length 168; Best Local Similarity 66.7%; Pred. No. 0.37; Matches 8; Conservative 0; Mismatches 4: Indela
                                                                                                                                                                                            Score 56; DB 2; Length 168;
Pred. No. 0.37;
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                                                                                                                                                                                                                                                Indels
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Eukaryota, Alveolata; Apicomplexa; Coccidia; Eimeriida;
Cryptosporidiidae; Cryptosporidium.
NCBI_TaxID=5807;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cryptosporidium parvum.
Bukaryota, Alveolata, Apicomplexa, Coccidia, Bimeriida,
Cryptosporidiidae, Cryptosporidium.
NCBI_TaxID=5807;
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                                                                                                                           168 168 MW; 2D02BC437C2AA44D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Thrombospondin-related adhesive protein (Fragment).
                                                                                                                                                                                                                   Pred. No. 0.37;
0; Mismatches
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Interpro; IPR00884; TSP1.
Pfam; PF00090; TSP 1; 2.
SMART; SM00209; TSP1; 3.
PROSITE; PS50092; TSP1; 3.
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                                                                                                                                                                                                                                                     Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
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Search completed: April 1, 2005, 13:59:21 Job time : 78.6522 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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OM protein - protein search, using sw model

Run on:

April 1, 2005, 13:43:07; Search time 16.6957 Seconds (without alignments) 69.156 Million cell updates/sec

US-09-462-909D-7 62 Title: Perfect score:

1 WSXWSXCSXXCG 12 Sequence: BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283416 seqs, 96216763 residues Searched:

Potal number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

PIR 79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	hypothetical prote	hypothetical prote	antigen Em100 - Ei	hypothetical prote	angiogenesis inhib	ပ္	protein CTRP - mal	hypothetical prote		F-spondin - rat	hypothetical prote	thrombospondin 1 p	thrombospondin 1 p	N	N	thrombospondin pre	cartilage intermed	brain-specific and	hypothetical prote	brain-specific ang	coccidiosis-relate	hypothetical prote	immunodominant mic	semaphorin F precu	hypothetical prote	TRAP-C2 protein -	hypothetical prote	etical	unc-5 protein - Ca
SUMMARIES	. QI	T16892	T29247	A48569	T00326	T18856	T00028	T18397	T25061	A47723	A38152	T15976	TSHUP1	A40558	TSHUP2	A42587	A39804	T09484	T00026	T34212	T00027	A45517	T16761	A45638	JC5928	T22545	S49108	T16557	T19477	T32541
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æ	Query	91.9	90.3	90.3	90.3	90.3	90.3	90.3	88.7	88.7	88.7	88.7	88.7	88.7	88.7	88.7	88.7	88.7	88.7	87.1	87.1	85.5	85.5	85.5	85.5	83.9	82.3	82.3	82.3	82.3
	Score	57	99	99	26	26	99	26	52	55	52	55	52	55	55	55	52	55	55	54	54	23	53	23	53	52	51	51	51	21
	Result No.	7	73	e	4	S	9	7	8		10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	29

	unc-5 protein, lon	hypothetical prote	thrombospondin-rel	sporozoite surface	hypothetical prote	hypothetical prote	hypothetical prote	hypothetical prote	properdin precurso	hypothetical prote	sporozoite, surface	hypothetical prote	gene ADAMTS-1 prot	hypothetical prote	protein F11C7.2 [i	properdin - mouse
•	B44294	T33922	S04531	A46283	T19366	T21064	T32570	T21371	829126	T47158	A45559	T00355	T00017	T00260	D89753	S05478
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	947	1360	559	574	736	2761	324	2165	469	220	826	837	951	951	152	437
	82.3	82.3	90.6	90.6	90.6	79.0	75.8	75.8	74.2	74.2	74.2	74.2	74.2	72.6	71.0	71.0
	21	21	20	20	20	49	47	47	46	46	46	46	46	45	44	44
	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

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hypochetical protein T19D2.1 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
C;Accession: T16892
R;Bentley.
Bubmitted to the EMBL Data Library, December 1995
A;Description: The sequence of C. elegans cosmid T19D2.
A;Reference number: Z18599
A;Accession: T16892
A;Accession: T16892
A;Accession: T16892
A;Molecule type: DNA
A;Molecule type: DNA
A;Molecule type: DNA
A;Accession: C;Genetics: C;Genetic
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A;Introne: 56/3; 96/1; 171/3; 199/3; 245/2; 293/2; 335/3; 395/3; 426/3; 484/2; 505/3; 585
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Pred. No. 0.21;
0; Mismatches 4; Indels
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Best Local Similarity 66.7%;
Matches 8; Conservative
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RESULT 1
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C;Species: Caenorhabditis elegans C;Date: j5-Oct_1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004 hypothetical protein F09F9.4 - Caenorhabditis elegans

Cyaccession: T29247
Rydinx, P.; Hawkins, J.
Submitted to the EMBL Data Library, November 1995
A;Pescription: The sequence of C. elegans cosmid F09F9.
A;Reference number: Z20594
A;Accession: T29247
A;Accession: T29247
A;Accession: T29247
A;Accession: L29247
A;Accession: L29247
A;Accession: L29247
A;Accession: L29247
A;Catus: preliminary; translated from GB/EMBL/DDBJ
A;Rossious: 1-654 cMIN>
A;Rossious: 1-654 cMIN>
A;Conetion: Company Co

A;Gene: CESP:F09F9.4 A;Introns: 89/3; 138/3; 192/3; 260/1; 312/1; 400/2; 445/3; 496/1; 523/1; 558/2; 596/2

ö 0; Gaps Score 56; DB 2; Length 654; Pred. No. 0.24; 0; Mismatches 4; Indels Query Match 90.3%; Best Local Similarity 66.7%; Matches 8; Conservative

1 WSXWSXCSXXCG 12

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A.Residues: 1-1444 <WIL>
A.Cross-references: UNIPROT: Q8MYA8; EMBL: Z50004; PIDN: CAA90293.1; GSPDB: GN00028; CESP: CO
                                                                                                                                                                                                                                                                                             R;McWurray, A.

submitted to the EMBL Data Library, July 1995
A;Reference number: 219917
A;Recession: 1724653
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Rocies type: DNA
A;Residues: 1-1444 (*M12>
A;Cross-references: EMBL:250006; PIDN:CAA90302.1; GSPDB:GN00028; CESP:C02B4.1
A;Experimental source: clone T07C5
                    A;Reference number: Z19031
A;Accession: T18856
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
submitted to the EMBL Data Library, July 1995
                                                                                                                                                                                                                                                                    A; Experimental source: clone C02B4
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                                                                                                                                                                                                                                                                                    C;Species: Eimeria maxima
C;Date: 01-Dec-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
C;Accession: A48569
K;Pasamontes, L.; Hug, D.; Humbelin, M.; Weber, G.
Mol. Biochem. Parasitol. 57, 171-174, 1993
A;Title: Sequence of a major Eimeria maxima antigen homologous to the Eimeria tenella mi
A;Reference number: A48569; MUID:93149203; PMID:8426611
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
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C;Species: Genorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T18856; T24653
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Reaidues: 1724 ePASS.
A; Reaidues: 1724 ePASS.
A; Cross-references: UNIPROT:Q04588; GB:M99058; NID:g158890; PID:g158891
A; Note: Sequence extracted from NCB1 backbone (NCBIN:123776, NCBIP:123777)
F; 45-218/Domain: von Willebrand factor type A repeat homology «TMR1»
F; 238-296/Domain: thrombospondin type I repeat homology «THR2»
F; 309-371/Domain: thrombospondin type I repeat homology «THR3»
F; 313-373/Domain: thrombospondin type I repeat homology «THR3»
F; 434-493/Domain: thrombospondin type I repeat homology «THR3»
F; 494-556/Domain: thrombospondin type I repeat homology «THR6»
F; 560-610/Domain: thrombospondin type I repeat homology «THR6»
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Pred. No. 0.33;
0; Mismatches 4; Indels
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Best Local Similarity 66.7%;
Matches 8; Conservative
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A48569
antigen Em100 - Eimeria maxima
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                            322 WSEWSACSETCG 333
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Les 8, Conservative
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A, Status: preliminary
A, Molecule type: nucleic acid
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Best Local
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C;Accession: T00028
R;Shiratsuchi, T.; Nishimori, H.; Ichise, H.; Nakamura, Y.; Tokino, T.
Cytogenet. Cell Genet. 79, 103-108, 1997
A;Title: Cloning and characterization of BAI2 and BAI3, novel genes homologous to brain-s
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          protein CTRP - malaria parasite (Plasmodium falciparum)
c;Species: Plasmodium falciparum
c;Species: Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T18397
C;Accession: T18397
Mol. Biochem. Parasitol. 74, 129-142, 1995
A;Title: Molecular cloning of a gene from Plasmodium falciparum that codes for a protein A;Reference number: Z18926; MUID:96360471; PMID:8719155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Cross-references: UNIPROT: 060242; EMBL: AB005299; NID: 93021700; PIDN: BAA25363.1; PID: 93(1 A; Experimental source: brain
A;Introns: 25/3; 70/3; 96/3; 139/3; 187/1; 234/2; 282/3; 376/2; 422/2; 478/3; 509/3; 566,
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N.Alternate names: BAI3 protein
C.Species: Homo sapiens (man)
C.Species: 22-Jan-1999 #sequence_revision 22-Jan-1999 #text_change 09-Jul-2004
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                                                                          Query Match
90.3%; Score 56; DB 2; Length 1444;
Best Local Similarity 66.7%; Pred. No. 0.43;
Matches 8; Conservative 0; Mismatches 4; Indels
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A; Map position: 6412-6412
F;344-398/Domain: thrombospondin type 1 repeat homology <THR3>
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A;Molecule type: mRNA
A;Residues: 1-1522 <8HI>
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R;Klar, A.; Baldassare, M.; Jessell, T.M.
Cell 69, 95-110, 1992
A;Title: F-spondin: a gene expressed at high levels in the floor plate encodes a secreted
A;Reference number: A38152; MUID:92208952; PMID:1555244
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C;Species: Homo sapiens (man)
C;Daces: 23-Aug-1997 #sequence revision 03-Aug-1995 #text_change 09-Jul-2004
C;Accession: A26155, A34274; A30140; A25812; A05172; A42927
R;Lawler, J; Hynes, R.O.
J. Cell Biol. 103, 1655-1648, 1986
A;Title: The structure of human thrombospondin, an adhesive glycoprotein with multiple cs
A;Reference number: A26155; MUID:87057617; PMID:2430973
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A;Introns: 23/1; 135/3; 220/3; 285/3; 325/2; 376/3; 461/2; 498/3; 532/3; 627/2; 714/1; 7:
                                                                                                                                                                                                                                                                                                                        ;Molecule_type: mRNA
:Residues: 1-807 <KLA>
:Cross-references: UNIPROT:P35446; GB:M88469; NID:g204176; PIDN:AAA41174.1; PID:g204177
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A;Experimental source: strain Bristol N2
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C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
C;Accession: T15976
                                                                                    Date: 04-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
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                                                                                                                                                                                                                                                                                                                                                                                                         A; Experimental source: embryo floor plate
A; Note: sequence extracted from NCBI backbone (NCBIN:90877, NCBIP:90878)
C; Superfamily: F-spondin; thrombospondin type 1 repeat homology (THR2)
F; 500-555/Domain: thrombospondin type 1 repeat homology (THR3)
F; 557-611/Domain: thrombospondin type 1 repeat homology (THR4)
F; 657-611/Domain: thrombospondin type 1 repeat homology (THR4)
F; 667-7121/Domain: thrombospondin type 1 repeat homology (THR5)
F; 667-7121/Domain: thrombospondin type 1 repeat homology (THR5)
F; 667-721/Domain: thrombospondin type 1 repeat homology (THR5)
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A;Molecule type: DNA
A;Residues: 1-957 <BEN>
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Pred. No. 0.4;
0; Mismatches
                                                               Species: Rattus norvegicus (Norway rat)
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66.7%;
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Best Local Similarity 66.7
Matches 8; Conservative
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Best Local Similarity
Matches 8; Conserva
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                                                                                                                      Accession: A38152
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Csupertamally: F-spondin; thrombospondin type 1 repeat homology
F;435-489/Domain: thrombospondin type 1 repeat homology <THR2>
F;607-662/Domain: thrombospondin type 1 repeat homology <THR1>
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A;Experimental source: clone T21B6
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Proc. Natl. Acad. Sci. US.A. 90, 8268-8272, 1993
A;Title: Ectopic neural expression of a floor plate marker in frog embryos injected with
A;Reference number: A47723; MUID:93376785; PMID:8367492
                                                                                                                   A;Cross-references: UNIPROT:Q25757; EMBL:U34363; NID:g1098897; PID:g1098898; PIDN:AAC469
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 hypothetical protein T21B6.3 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct.1999 #sequence_revision 15-Oct.1999 #text_change 09-Jul-2004
C;Accession: T25061
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         F-spondin precursor - African clawed frog
C;Species: Kanopus laevis (African clawed frog)
C;Date: 27-Jun-1994 #sequence_revision 27-Jun-1994 #text_change 09-Jul-2004
C;Accession: A47723
                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                   Score 56; DB 2; Length 2098;
Pred. No. 0.57;
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Pred. No. 0.4;
0; Mismatches 4; Indels
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                              preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Introns: 20/1; 47/1; 76/1; 152/1; 735/2; 754/2
                                                                                                                                                                                                                                      0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Mismatches
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66.78;
                                                                                                                                                                      Query Match
Best Local Similarity 66.7%;
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                1644 WSDWSSCSKTCG 1655
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Matches 8; Conservative
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                                                      A; Molecule type: DNA
A; Residues: 1-2098 <TRO>
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Best Local Similarity
Matches 8; Conserv
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Residues: 1-803 <RUI>
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A; Accession: T18397
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Gaps

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Title: Expression and initial characterization of recombinant mouse thrombospondin 1 ar ; Title: Expression and initial characterization of recombinant mouse. S68787; MUID:96234006; PMID:8654563; Accession: S68787
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A, Residues: 19-26, XY, 28-37 < CHB>
A, Residues: 19-26, XY, 28-37 < CHB>
A, Residues: 19-26, XY, 28-37 < CHB>
C, Complex: homotrimer, disulfide linked
C, Superfamily: thrombospondin 1, EGF homology; thrombospondin type 1 repeat homology; vor C, Keywords: calcium binding; glycoprotein; homotrimer
C, Keywords: calcium binding; glycoprotein; homotrimer
F; 11-18/Domain: signal sequence #status predicted < SIG>
F; 19-1170/Product: thrombospondin 1 #status predicted < AMT>
F; 378-429/Domain: thrombospondin type 1 repeat homology < THR1>
F; 434-490/Domain: thrombospondin type 1 repeat homology < THR2>
F; 431-547/Domain: thrombospondin type 1 repeat homology < THR3>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Cross-references: GB:J05605; GB:J05606; NID:G201991; PIDN:AAA40431.1; PID:G554390; Laherty, C.D.; O'Rourke, K.; Wolf, F.W.; Katz, R.; Seldin, M.F.; Dixit, V.M. B.Ol. Chem. 267, 3274-3281, 1992
T. Biol. Chem. 267, 3274-3281, 1992
Tyritle: Characterization of mouse thrombospondin 2 sequence and expression during cell; Reference number: A42587; MUID:92147683; PMID:1371115
                                                                                                                                                                                                                                                                                                                                                 thrombospondin 1 precursor - mouse
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Accession: 6-Jun-1992 #sequence revision 05-Jun-1992 #text_change 09-Jul-2004
C;Accession: A40558; A37905; B42587; S68787
R;Lawler, J.; Duquette, M.; Ferro, P.; Copeland, N.G.; Gilbert, D.J.; Jenkins, N.A.
Genomics 11, S87-G00, 1991
A;Title: Characterization of the murine thrombospondin gene.
A;Reference number: A40558; MUID:92128941; PMID:1774063
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F;248,360,708,1067/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ,Status: preliminary; not compared with conceptual translation; Molecule type: mRNA, Residues: 1-1152, 'P', 1154-1170 <LAH>, Residues: 1-168: M87276
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Indels
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Pred. No. 0.52;
0; Mismatches
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66.7%;
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                                                                                                                                                          441 WSPWSSCSVTCG 452
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    8; Conservative
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Best Local Similarity
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Status: preliminary
Molecule type: DNA
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        Matches
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Ajnucions and period processes and adhesion, and in platelet aggregation complex: homotrimer, disulfide linked

CjComplex: homotospondin 1; EGF homology; thrombospondin type listatus predicted calls

Fill-18/Domain: son Willebrand factor type Crepeat homology cWG>

Fill-18/Domain: thrombospondin type listatus homology cTHR2>

Fill-286/Domain: thrombospondin type listatus homology cTHR2>

Fill-286/Domain: EGF homology cEGF2>

Fill-286/Domain: EGF homology cEGF2>

Fill-286/Domain: EGF homology cEGF2>
                                                                                                                                                                                                                                                                                                                         A,Accession: A34274
A,Molecule type: DNA
A,Roslecule type: DNA
A,Cross-references: GB:J04835
A,Cross-references: GB:J04835
R;Hennessy, S.W.; Frazier, B.A.; Kim, D.D.; Deckwerth, T.L.; Baumgartel, D.M.; Rotwein,
A,Title: Complete thrombospondin mRNA sequence includes potential regulatory sites in th
A,Reference number: A30140; MUID:89139590; PMID:2918029
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Accession: A30140
A;Molecule type: mRNA
A;Note: parts of this sequence, including the amino end of the mature protein, were dete
B;Kobayashi, S.; Bden-McCucchan, F.; Framson, P.; Bornstein, P.
Biochemistry 25, 8418-8425, 1986
A;Title: Partial amino acid sequence of human thrombospondin as determined by analysis of A;Reference number: A25812; MUID:87157592; PMID:3030396
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Molecule type: mRNA
A; Residues: 1-83, 74, 76, 701X>
A; Residues: 1-83, 74, 76, 701X>
A; Cross-references: GB:M1436; NID:9340005; PIDN; AAA61237, 1; PID:9553801
A; Note: parts of this sequence, including the amino end of the mature protein, were dete
R; Sun, X.; Skorstengaard, K.; Mosher, D.F.
Cell Biol. 118, 693-7701, 1935
A; Title: Disulfides modulate RGD-inhibitable cell adhesive activity of thrombospondin.
A; Reference number: A42927; MUID:92348511; PMID:1379247
        A; Molecule type: mRNA
A; Residues: 1-1170 <LAM's
A; Cross-references: UNIPROT: P07996; GB:X04665; NID: G37137; PIDN: CAA28370.1; PID: G37138
A; Note: parts of this sequence, including the amino end of the mature protein, were dete
R; Laherty, C.D.; Gierman, T.M.; Dixit, V.M.
B; Dixit, Chem. 264, 11222-11227, 1989
A; Title: Characterization of the promoter region of the human thrombospondin gene. DNA & A; Reference number: A34274; MUID: 89291870; PMID: 2544587
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F;171-232/Disulfide bonds: #status predicted
F;171-237/Disulfide bonds: attactor predicted
F;270,274/Disulfide bonds: interchain #status predicted
F;210,274/Disulfide bonds: interchain #status predicted
F;610/Modified site: erythro-beta-hydroxyasparagine (Asn) #status predicted
F;1051/Binding site: carbohydrate (Asn) (covalent) #status absent
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A; Molecule type: mRNA
A; Molecule type: mRNA
A; Cross-teferences: 1-83, 'A', 485-397 < KOB>
A; Cross-references: GB: M25631; NID: 9538353; PIDN: AAA36741.1; PID: 9538354
A; Cross-teferences: GB: M25631; NID: 9538353; PIDN: AAA36741.1; PID: 9538354
R; Dixit, V. M.; Hennessy, S. W.; Grant, G.A.; Rotwein, P.; Frazier, W.A.
Proc. Natl. Acad. Sci. U.S.A. 83, 5449-5453, 1986
A; Reference number: A05172; MUID: 86287276; PMID: 3461443
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Pred. No. 0.52;
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A,Residues: 987-1003 «SUN»
A,Note: Cys-992 is shown to have a free sulfhydryl
C,Genetics:
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A)Cross-references: GDB:120438; OMIM:188060
A,Map position: 15q15-15q15
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Best Local Similarity
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Best Local Similarity 66.7
Matches 8; Conservative
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                                                                                                                                                       A;Residues: 1-873 <BOR>
                                                               A;Status: preliminary A;Molecule type: mRNA
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C;Date::19-May-1995 #sequence_revision 03-Aug-1995 #text_change 09-Jul-2004
C;Accession: A47379; A42173
R;LaBell, T.L.; Byers, P.H.
Genomics 17, 225-229, 1993
A;Title: Sequence and characterization of the complete human thrombospondin 2 cDNA: pote A;Reference and characterization Pylones Pylones
                                                                                                                                                                                                                                                                                                                                                                              A; Molecule type: mRNA
A; Residues: 1-1172 < LAB>
A; Ross-references: UNTPROT: P35442; GB: L12350; NID: G307505; PIDN: AAA03703.1; PID: G307506
R; LaBell, T.L.; Milewicz, D.J.; Disteche, C.M.; Byers, P.H.
Genomics 12, 421-429, 1992
A; Title: Thrombospondin II: partial cDNA sequence, chromosome location, and expression cA; Reference number: A42173; MUID: 92217961; PMID: 1559694
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A42587

thrombospondin 2 precursor - mouse

c;Species Mus musculus (house mouse)

C;Species Musculus (house mouse)

C;Date: 04-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004

C;Accession: A42587; A39851

C;Accession: A42587; A39851

C;Accession: A42587; Molf, F.W.; Katz, R.; Seldin, M.F.; Dixit, V.M., J. Biol. Chem. 267, 3274-3281, 1992

A;Title: Characterization of mouse thrombospondin 2 sequence and expression during cell
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A; Residues: 1-172 - LAH3
A; Cross-references: UNIPROT:003350; GB:L07803; GB:M87275; NID:g340421; PIDN:AAA53064.1;
A; Note: sequence extracted from NCBI backbone (NCBIP:81502)
R; Bornstein, P.; O'Rourke, K.; Wikstrom, K.; Wolf, F.W.; Katz, R.; Li, P.; Dixit, V.M.
A; Biol. Chem. 2566, 12821-12824, 1991
A; Title: A second, expressed thrombospondin gene (Thbs2) exists in the mouse genome.
A; Reference number: A39851; MUID:91302287; PMID:1712771
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Experimental source: fibroblast
A;Note: sequence extracted from NCBI backbone (NCBIN:95091, NCBIP:95096)
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
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Pred. No. 0.52;
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A, Status: preliminary; not compared with conceptual translation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A,Gene: GDB:THBS2; TSP2
A,Cross-references: GDB:128789; OMIM:188061
A,Map position: 6427-6427
G,Complex: homotrimer, disulfide linked
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 66.7%;
Matches 8; Conservative
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A,Molecule type: mRMAA,
Residues: 560-1172 <LA2>
A,Cross-references: GB:M81339
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A/Cross-references: GB:W64866; NID:g201994; PIDN:AAA40432.1; PID:g201995
C;Superfamily: thrombospondin 1; EGF homology; thrombospondin type 1 repeat homology; voi
C;Superfamily: thrombospondin 1; EGF homology; thrombospondin type 1 repeat homology <VWC>
F;319-377/Domain: von Willebrand factor type C repeat homology <VWC>
F;380-431/Domain: thrombospondin type 1 repeat homology <THR1>
F;436-497/Domain: thrombospondin type 1 repeat homology <THR2>
F;53-549/Domain: thrombospondin type 1 repeat homology <THR3>
F;55-588/Domain: EGF homology <EGF>
F;652-691/Domain: EGF homology <EGF>
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A:Accession: A39851
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Gaps ö

1, 2005, 14:00:30

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April 1, 2005, 13:59:39 ; Search time 61.8261 Seconds (without alignments) 64.360 Million cell updates/sec
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6/ptodata/2/pubpaa/USO9C PUBCOMB.ppp:
6/ptodata/2/pubpaa/USO9 NEW PUB.ppp:
6/ptodata/2/pubpaa/USIOA PUBCOMB.ppp:
6/ptodata/2/pubpaa/USIOC PUBCOMB.ppp:
6/ptodata/2/pubpaa/USIOC PUBCOMB.ppp:
6/ptodata/2/pubpaa/USIOC PUBCOMB.ppp:
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6/ptodata/2/pubpas/PCT NEW PUB.pep;
6/ptodata/2/pubpas/USO6_PUBCOMB.pep;
6/ptodata/2/pubpas/USO7_NEW PUB.pep;
6/ptodata/2/pubpas/PCTUG_PUBCOMB.pep;
6/ptodata/2/pubpas/PCTUG_PUBCOMB.pep;
6/ptodata/2/pubpas/USO8_NEW PUB.pep;
6/ptodata/2/pubpas/USO8_PUBCOMB.pep;
6/ptodata/2/pubpas/USO8_PUBCOMB.pep;
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/cgn2_6/ptodata/2/pubpaa/US10D_PUBCOMB.pep
/cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:
/cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep:
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/cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:
GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
                                                                                                           OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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Perfect score:
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					SUMMARIES		
Result		Query	* Query				
No.	Score	Match	Length	80	ID	Description	
7	57	91.9	1077	15	S US-10-190-115-43	Sequence 43, Appl	
7	5	91.9		15	US-10-369-072-43	Sequence 43, Appl	
М	99	56 90.3		15	US-10-019-065A-21	Sequence 21, Appl	
4	26	90.3		11	US-09-939-853A-96	Sequence 96, Appl	
S	26	90.3		0	US-09-918-171A-7	Sequence 7, Appli	
9	26	90.3		10	US-09-981-151A-32	Sequence 32, Appl	
7	99	90.3	997	16	US-10-408-765A-1094	Sequence 1094, Ap	
æ	26	90.3		15	US-10-312-352-23	Sequence 23, Appl	
6	26	90.3		14	US-10-225-567A-346	Sequence 346, App	
10	99	90.3		15	US-10-386-414-2	Sequence 2, Appli	
11	26	90.3	٠.	σ	US-09-788-043C-5	Sequence 5, Appli	
12	26	90.3	•	14	US-10-213-509-5	Sequence 5, Appli	
13	26	90.3	•	15	US-10-085-198-2	Sequence 2, Appli	

Sequence 12, Appl Sequence 406, App Sequence 13, Appl Sequence 14, Appl Sequence 10, Appl Sequence 10, Appl Sequence 5, Appl Sequence 5, Appl Sequence 10, Appl Sequence 10, Appl Sequence 21, Appl Sequence 22, Appl Sequence 23, Appl Sequence 24, Appl Sequence 24, Appl Sequence 27, Appl Sequence 27, Appl Sequence 27, Appl Sequence 1106, Appl Sequence 1106, Appl Sequence 1106, Appl Sequence 1106, Appl Sequence 11, Appl Sequence 1, Appl Sequence 2, Appl Sequence 1, Appl Sequence 2, Appl Sequence 1, Appl Sequence 2, Appl Sequence 3, Appl Sequence 2, Appl Sequence 3, Appl Sequenc	128,
US-10-042-696-12 US-10-074-978A-408 US-10-019-065A-14 US-10-019-065A-14 US-10-019-065A-14 US-10-019-065A-14 US-10-019-065A-14 US-10-019-065A-7 US-10-019-065A-7 US-10-019-065A-7 US-09-802-094-6 US-09-802-094-6 US-09-802-094-6 US-09-989-687-7 US-09-989-687-10 US-09-989-687-10 US-10-296-733-22 US-10-296-733-27 US-10-296-733-27 US-10-296-733-27 US-10-296-733-27 US-10-19-065A-32 US-10-036-869-1 US-09-919-603-7 US-09-919-603-7 US-09-919-603-7 US-09-919-603-7 US-09-919-603-7 US-09-919-603-7 US-09-919-603-7 US-09-919-603-7	10-161-493-12
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ALIGNMENTS

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US-10-190-115-43

Sequence 43, Application US/10190115

Publication No. US2003020394A1

GENERAL INFORMATION:
APPLICANT: Aleobrook, John P. II
APPLICANT: Gasman, Stacie J.
APPLICANT: Gasman, Stacie J.
APPLICANT: Gasman, Stacie J.
APPLICANT: Gase, William M.
APPLICANT: Gase, William M.
APPLICANT: Gase, William M.
APPLICANT: Gase, William M.
APPLICANT: Liu, Xiaohong
APPLICANT: Liu, Xiaohong
APPLICANT: Liu, Xiaohong
APPLICANT: Padigaru, Muralidhara
APPLICANT: Padigaru, Muralidhara
APPLICANT: Padigaru, Meera
APPLICANT: Shimkets, Richard A.
APPLICANT: Shimkets, Richard A.
APPLICANT: Shimkets, Richard A.
APPLICANT: Speeres, Edward S. Jr.
APPLICANT: Speeres, Edward S. Jr.
APPLICANT: Tangier, Raymond J. Jr.
APPLICAN
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Sequence 96, Application US/09939853A
Sequence 96, Application US/09939853A
Publication No. US20040039163A1
GENERAL INFORMATION
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: No. US20040039163A1e1 Proteins and Nucleic Acids Encoding Same
FILE REFERENCE: 21402-099
CURRENT APPLICATION NUMBER: US/09/939,853A
CURRENT FILING DATE: 2001-08-27
PRIOR FILING DATE: 2000-08-25
REIOR FILING DATE: 2000-08-25
REIOR FILING DATE: 2001-02-09
PRIOR FILING DATE: 2001-02-20
PRIOR PLING DATE: 2001-02-20
PRIOR APPLICATION NUMBER: 60/269,961
PRIOR PLING DATE: 2001-02-20
PRIOR APPLICATION NUMBER: 60/277,337
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US-10-019-065A-21

Sequence 21, Application US/10019065A

PUDLICATION NO. US20040086501A1

GENERAL INFORMATION:

APPLICANT: Bayer Corporation

TITLE OF INVENTION: Proporation

TITLE OF INVENTION: PROPORATION:

CURRENT PILIANG DATE: 2002-08-30

PRIOR APPLICATION NUMBER: US/10/019,065A

CURRENT PILING DATE: 2000-03-31

NUMBER: OF SEQ ID NOS: 34

SOFTWARE: PatentIn version 3.1

SEQ ID NO 21

LENGTH: 52
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                          PRIOR APPLICATION NUMBER: 60/216,722
PRIOR FILING DATE: 2000-07-07
PRIOR FILING DATE: 2000-07-07
PRIOR FILING DATE: 2000-07-17
PRIOR FILING DATE: 2000-07-17
PRIOR FILING DATE: 2000-07-17
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 100
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 43
LENGTH: 1077
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OTHER INFORMATION: Isolated type 1 thrombospondin domain sequence
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Pred. No. 0.97;
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Pred. No. (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 90.3%;
Best Local Similarity 66.7%;
Matches 8; Conservative
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nilarity 66.7%;
Conservative
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CRGANISM: Mus musculus
US-10-369-072-43
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Matches 8; Conserv
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Shimkets, Richard
Padigaru, Muralidhara
EBNION: No. US20040014081Alel Proteins and Nucleic Acids Encoding Same
NCE: 21402-050 CON2
PRIOR APPLICATION NUMBER: 60/386,816
PRIOR FILING DATE: 2002-06-07
PRIOR FILING DATE: 2002-06-07
PRIOR PEDICATION NUMBER: 60/215,854
PRIOR PILING DATE: 2000-07-03
PRIOR APPLICATION NUMBER: 60/215,902
PRIOR PILING DATE: 2000-07-03
PRIOR PILING DATE: 2000-07-03
PRIOR PILING DATE: 2000-07-03
PRIOR PILING DATE: 2000-07-07
PRIOR APPLICATION NUMBER: 60/216,585,
PRIOR PILING DATE: 2000-07-07
PRIOR PAPLICATION NUMBER: 60/216,586
PRIOR PILING DATE: 2000-07-07
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Pred. No. 6
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R APPLICATION NUMBER: 09/898,994

R FILING DATE: 2001-07-03

R FILING DATE: 2000-07-03

R FILING DATE: 2000-07-03

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PRIOR PELLING DATE: 2003-02-18
PRIOR FILLING DATE: 2003-02-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 43, Application US/10369072 Publication No. US20040014081A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Alsobrook II, John P
APPLICANT: Spaderna, Stephen K
APPLICANT: Tchernev, Velizar
APPLICANT: Liu, Xiaohong
APPLICANT: Shenoy, Suresh
APPLICANT: Spytek, Kimberly
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Lepley, Denise M
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Taupier, Raymond T
Ragtelli, Luca
Grosse, William M
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Best Local Similarity
Matches 8; Conserv
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LENGTH: 1077
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HENCRANI FILING DATE: 2001-10-16

PRICA APPLICATION NUMBER: 60/241,040

PRICA PAPLICATION NUMBER: 60/241,063

PRICA APPLICATION NUMBER: 60/241,063

PRICA RILING DATE: 2000-10-17

PRICA RILING DATE: 2000-10-17

PRICA PLING DATE: 2000-10-17

PRICA PAPLICATION NUMBER: 60/241,243

PRICA PLING DATE: 2000-10-17

PRICA PAPLICATION NUMBER: 60/242,152

PRICA PAPLICATION NUMBER: 60/242,482

PRICA PAPLICATION NUMBER: 60/242,611

PRICA PAPLICATION NUMBER: 60/242,611

PRICA PAPLICATION NUMBER: 60/242,611

PRICA PAPLICATION NUMBER: 60/242,611

PRICA PAPLICATION NUMBER: 60/242,612

PRICA PAPLICATION NUMBER: 60/242,880

PRICA PAPLICATION NUMBER: 60/242,880

PRICA PAPLICATION NUMBER: 60/242,880

PRICA PAPLICATION NUMBER: 60/242,881

PRICA PAPLICATION NUMBER: 60/242,881
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APPLICANT: Glason, Bradford W.
APPLICANT: dibson, Bradford W.
APPLICANT: dibson, Bradford W.
APPLICANT: diblor, Gary M.
APPLICANT: Warnock, Dale E.
TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION
TITLE OF INVENTION: IDENTIFIED IN THE MITOCHONDRIAL PROTEOME
FILE REFERENCE: 660088.465
CURRENT APPLICATION NUMBER: US/10/408,765A
CURRENT FILING DATE: 2003-04-04
NUMBER OF SEQ ID NOS: 3077
SOFTWARE FARESEQ for Windows Version 4.0
SEQ ID NO 1094
LENGTH: 997
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Pred. No. 8.2;
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                        APPLICANT: Fernandes, Elma R
APPLICANT: Gorman, Linda
TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
FILE REFERENCE: 21402-168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Mismatches
                                                                                                                    CURRENT APPLICATION NUMBER: US/09/981,151A CURRENT FILING DATE: 2001-10-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 1094, Application US/10408765A Publication No. US20040101874A1 GENERAL INFORMATION:
APPLICANT: Ghosh, Soumitra S. APPLICANT: Fahy, Boin D.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 32
LENGTH: 997
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Matches 8; Conservative
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US-10-408-765A-1094
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ORGANISM: Homo sapiens
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Best Local Similarity
Matches 8; Conserv
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US-09-918-171A-7.
Sequence 7, Application US/09918171A
Sequence 7, Application US/09918171A
Sequence 7, Application US/09918171A
Setent No. US20020110894A1
Setent No. US20020110894A1
APPLICANT: Hurskainen, Tiina L.
APPLICANT: Hurskainen, Tiina L.
APPLICANT: Hirohata, Satoshi
TITLE OF INVENTION: Nucleic Acids Encoding Zinc Metalloproteases
FILE REPERENCE: 26473/04193
CURRENT FILING DATE: 2001-07-30
PRIOR PILING DATE: 1999-08-06
NUMBER: 09/369,364
PRIOR FILING DATE: 1999-08-06
NUMBER: 09/369,364
PRIOR FILING DATE: 1999-08-06
SEQ ID NO 7
LENGTH: 997
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Pred. No. 8.2;
0; Mismatches
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                                                              Ellerman, Karen
Shimkets, Richard A
Padigaru, Muralidhara
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Patturajan, Meera
Taupier Jr, Raymond J
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ORGANISM: Homo sapiens ADAMTS-7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Edinger, Shlomit R
APPLICANT: Gerlach, Valerie
APPLICANT: MacBougall, John R
APPLICANT: Smithson, Glennda
                                                                                                                                                                                                         90.3%;
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Spytek, Kimberly A
PRIOR FILING DATE: 2001-03-20
NUMBER OF SEQ ID NOS: 159
SOFTWARE: PatentIn Ver. 2.1
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Peyman, John A
Stone, David J
Gunther, Erik
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Best Local Similarity 60...
Best Local Similarity 60...
                                                                                                                                                                                                                                                                                                                                                     352 WSEWSDCSTSCG 363
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Best Local Similarity 66...
8; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-981-151A-32
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APPLICANT:
APPLICANT:
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                                                                                                                                                                                                                                                                                                        APPLICANT: INCYTE GENOMICS, INC.; TANG, Y. Tom
APPLICANT: WISH Henry; AZIMZAI, Yalda
APPLICANT: HE, Ann; BATRA,
APPLICANT: GINERILL, JOHD D.; MARCHOS, GFEGORY A.
APPLICANT: GINERILL, JOHD D.; MARCHOS, GFEGORY,
APPLICANT: GINERILL, JOHD D.; MARCHOS,
APPLICANT: GINERILL, JOHD D.; MARCHOS,
APPLICANT: GINERILL, AND Neal; YAO, MONIQUE G.
APPLICANT: GINERILL, MARIAH, R.; HARALIA, APPLICANT: GINERILL,
APPLICANT: GINERILL, MARIAH, R.; HARALIA, APPLICANT: GINERILL OF INTEGRO, JOHNE, J. J. A.
APPLICANT: GINERILL AND MARIAH, R.; HARALIA, APPLICANT: LU, YON, BANGHOWAR, Usaglapal APPLICANT: LEE, ERGEGERA, ALGIGCE, DEDORA A.
APPLICANT: WARREN, LEE, ERGEGERA, ALGIGCE, DEDORA A.
APPLICANT: WARREN, LEE, ERGEGERA, ALGIGCE, DEDORA A.
APPLICANT: WARREN, ARGEGERA, ALGIGCE, DEDORA A.
APPLICANT: WARREN, ARGEGERA, ALGIGCE, DEDORA A.
APPLICANT: WARREN, ARGEGERA, ALGIGCE, ADBRESTON MOLECTIES
FILE REFERENCE: PP-0794 USN UNBER: US 60/219.462
PRIOR APPLICATION NUMBER: US 60/244.021
PRIOR APPLICATION NUMBER: US 60/249.570
PRIOR PRIOR PRIING DATE: 2000-11-16
SOUPHARM PRIOR PRIOR DATE: 2000-11-16
SOUPHARM PRIOR PRIOR DATE: 2000-11-16
LEMERY PRIOR PRIOR DATE: 2000-11-16
LEMERY PRIOR PRIOR DATE: 2000-11
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; OTHER INFORMATION: Incyte ID No. US20040053824A1 55022490CD1
US-10-312-352-23
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Pred. No. 9.7;
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                                                                                                                                                              RESULT 8
US-10-312-352-23
i Sequence 23, Application US/10312352
i Publication No. US20040053824A1
i GENERAL INFORMATION:
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Best Local Similarity 66.7
Matches 8; Conservative
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                                                           544 WSAWSICSRSCG 555
1 WSXWSXCSXXCG 12
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ORGANISM: Homo sapiens
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RESULT 9 US-10-225-567A-346 ; Sequence 346, Application US/10225567A

113 WSAWSICSRSCG 124

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PREMISEAL INFORMATION: GROUD-1994A.

REMEMBAL INFORMATION: GROCI-mores
APPLICANT HIRESPAN BOOCH-mores
APPLICANT HIRESPAN BOOCH-mores
APPLICANT HIRESPAN BOOCH-more
APPLICANT HIRESPAN BOOC
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Sequence 2, Application US/10085198
Publication No. US20040009907A1
GENERAL INFORMATION:
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ORGANISM: Artificial Sequence
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66.7%;
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Best Local Similarity 66.7
Matches 8, Conservative
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US-10-085-198-2
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| Sequence 5, Application US/09788043C
| Patent No. US20020107361A1
| GENERAL INFORMATION:
| APPLICANT: Heller, Renu
| APPLICANT: Allonowski, Paul
| TITLE OF INVENTION: Thrombospondin Domains and Nucleic Acid Compositions
| TITLE OF INVENTION: Thrombospondin Domains and Nucleic Acid Compositions
| TITLE OF INVENTION: Brocding the Same
| FILE REFERENCE: ROCH-004
| CURRENT APPLICATION NUMBER: 60/184,152
| PRIOR PAPLICATION NUMBER: 60/184,152
| PRIOR PAPLICATION NUMBER: 60/184,152
| NUMBER OF SEQ ID NOS: 10
| SOFTWARE: PastSEQ for Windows Version 4.0
| SEQ ID NO 5
| ERNOTH: 1690
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                                                              Score 56; DB 15; Length 1686;
Pred. No. 12;
0; Mismatches 4; Indels
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Pred. No. 12;
0; Mismatches 4; Indels
                                                                                                         4; Indels
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Publication No. US20030054485A1
GENERAL INFORMATION:
GENERAL INFORMATION:
THUR OF INVENTION: JELLY GENES AND THEIR USES
TITLE OF INVENTION: JELLY BELLY GENES AND THEIR USES
TITLE OF INVENTION: JELLY BELLY GENES AND THEIR USES
CURRENT APPLICATION NUMBER: US/10/213,509
CURRENT PILING DATE: 2002-08-06
PRIOR FILING DATE: 2001-08-09
NUMBER OF SEQ ID NOS: 5
SOFTWARE: FRAEKEQ for Mindows Version 4.0
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Pred. No. 23;
0; Mismatches
                                                                90.3%;
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                                                         Query Match
Best Local Similarity 66.7
Matches 8; Conservative
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Best Local Similarity 66.7
Matches 8; Conservative
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; ORGANISM: Homo Sapien
US-10-386-414-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; ORGANISM: H. sapiens
US-10-213-509-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
ORGANISM: human
                                                                                                                                                                                                                                                  RESULT 11
US-09-788-043C-5
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LENGTH: 4123
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US-10-213-509-5
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Best Local S
Matches 8
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Sequence 12, Application US/10042696
Publication No. US20030171298A1
GENERAL INFORMATION:
APPLICANT: TUSZYDSKi, George
APPLICANT: Williams, Taffy
APPLICANT: APPLICANT: APPLICANT: APPLICANT: TUSZYDSKi, George
APPLICANT: A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: synthetic fragment/analog of
OTHER INFORMATION: thrombospondin
US-10-042-696-12
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APPLICANT: Alsobrook et al.

TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
FILE REPERENCE: 21402-279

CURRENT APPLICATION NUMBER: 60/271,646

PRIOR PILING DATE: 2001-02-25

PRIOR PILING DATE: 2001-03-16

PRIOR PILING DATE: 2001-03-16

PRIOR PILING DATE: 2001-03-16

PRIOR PILING DATE: 2001-08-16

PRIOR PILING DATE: 2001-08-16

PRIOR PLING DATE: 2001-08-16

PRIOR PLING DATE: 2001-08-16

PRIOR PLING DATE: 2001-08-16

PRIOR PLING DATE: 2001-08-27

PRIOR PLING DATE: 2001-08-27

PRIOR PLING DATE: 2001-03-20

PRIOR PILING DATE: 2001-04-21

PRIOR PILING DATE: 2001-04-21

PRIOR PILING DATE: 2001-04-21

PRIOR PLING DATE: 2001-04-21

PRIOR PILING DATE: 2001-06-20

PRIOR PILING DATE: 2001-02-28

PRIOR PILING DATE: 2001-02-38

PRIOR PILING DATE: 2001-02-38
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Pred. No. 23;
0; Mismatches 4; Indels
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CURRENT FILING DATE: 2003-01-07

PRIOR APPLICATION NUMBER: 60/268,221

PRIOR APPLICATION NUMBER: 60/315,109

PRIOR FILING DATE: 2001-02-13

PRIOR PELING DATE: 2001-08-14

PRIOR PELING DATE: 2001-03-16

PRIOR PELING DATE: 2001-03-16

PRIOR PELING DATE: 2001-10-18

PRIOR PELING DATE: 2001-10-18

PRIOR PELING DATE: 2001-11-12

PRIOR PELING DATE: 2001-11-21

PRIOR PILING DATE: 2001-11-21

PRIOR PELING DATE: 2001-10-18

PRIOR PILING DATE: 2001-10-18

PRIOR PILING DATE: 2001-10-14

PRIOR PILING DATE: 2001-10-14

PRIOR PILING DATE: 2001-10-14

PRIOR PILING DATE: 2001-10-14

PRIOR PILING DATE: 2001-04-02

PRIOR PILING DATE: 2001-04-02

PRIOR PILING DATE: 2001-08-08

PRIOR PILING DATE: 2001-08-08

PRIOR PILING DATE: 2001-08-18

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PRIOR PELING DATE: 2001-08-18

PRIOR PELING
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APPLICANT: Milet, Isabelle
APPLICANT: Milet, Isabelle
APPLICANT: Seimen, John
TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING CURRENT APPLICATION NUMBER: US/10/074,978A
CURRENT RILING DATE: 2003-01-07
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Query Match

88.7%; Score 55; DB 14; Length 23;
Best Local Similarity 66.7%; Pred. No. 0.73;
Matches 8; Conservative 0; Mismatches 4; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 408, Application US/10074978A Publication No. US20040010119A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Leite, Mario
APPLICANT: Spytek, Kimberly A
APPLICANT: Guo, Xiaojia (Sasha)
APPLICANT: Fernandes, Elma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ichernev, Velizar T
Malyankar, Uriel M
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Kekuda, Ramesh
Liu, Xiahong
Casman, Stacie
Boldog, Ferenc
Patturajan, Meera
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Vernet, Corine
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Rastelli, Luca
Mezes, Peter S
Ellerman, Karen
Heyes, Melvin P
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US-10-074-978A-408
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; SEQ ID NO 408
; LENGTH: 41
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-074-978A-408

Query Match
Best Local Similarity 66.7%; Pred. No. 1.1;
Matches 8; Conservative 0; Mismatches 4; Indels 0; Gaps
Qy 1 WSXWSXCSXXCG 12
| | | | | | | | |
Db 3 WSLWSVCSXTCG 14
Search completed: April 1, 2005, 14:22:17
Job time: 63.8261 secs
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GenCore version 5.1.6 (c) 1993 - 2005 Compugen Ltd.
             Copyright
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OM protein - protein search, using sw model

Run on:

April 1, 2005, 13:44:22 ; Search time 21.1304 Seconds (without alignments) 42.393 Million cell updates/sec

US-09-462-909D-7 62 1 WSXWSXCSXXCG 12 Title: Perfect score: Sequence: BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

513545 segs, 74649064 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Issued Patents AA:* Database :

/cgnz_6/ptodata/1/laa/5A_COWB.pep:*
/cgnz_6/ptodata/1/laa/5B_COWB.pep:*
/cgnz_6/ptodata/1/laa/6A_COWB.pep:*
/cgnz_6/ptodata/1/laa/6A_COWB.pep:*
/cgnz_6/ptodata/1/laa/PCTUS_COMB.pep:*
/cgnz_6/ptodata/1/laa/PCTUS_COMB.pep:* £ 4 5 6

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Sequence 10, Appli Sequence 3, Appli Sequence 3, Appli Sequence 186, App Sequence 186, App Sequence 186, App Sequence 186, App Sequence 10, Appl Sequence 10, Appl Sequence 20, Appl Sequence 31, Appl Sequence 31, Appl Sequence 31, Appl Sequence 31, Appl Sequence 31, Appl Sequence 31, Appli Sequence 31, Appli Sequence 31, Appli Sequence 31, Appli Sequence 31, Appli Sequence 31, Appli
US-08-313-288B-10 US-09-132-769-1 US-09-132-769-3 US-09-132-769-5 US-09-132-769-5 US-09-713-550-186 US-09-713-550-186 US-09-970-966-186 US-09-970-966-186 US-09-949-016-11112 US-08-313-288B-20 US-08-313-288B-19 US-08-918-19-19-10-08-914-11 US-08-918-19-14-13-18-19-14-13-18-19-14-13-18-19-14-13-18-19-14-13-18-19-14-13-18-19-14-13-18-19-14-13-18-19-14-13-18-19-14-13-18-19-14-13-18-19-14-13-18-18-18-18-18-18-18-18-18-18-18-18-18-
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US-09-70-767-58094

Sequence 58094, Application US/09270767

Patent No. 6703491

GENERAL INFORMATION:

TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster

FILE REFRENCE: File Reference: 7326-094

CURRENT APPLICATION NUMBER: US/09/270,767

CURRENT PILING DATE: 1995-03-17

NUMBER OF SEQ ID NOS: 62517

SOFTWARE: PatentIN Ver. 2.0

SEQ ID NO 58094
                                        Sequence 46823, Application US/09270767

Batent No. 6703491

GENERAL INFORMATION:

APPLICANT: Homburger et al.

TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster FILE REPERENCE: File Reference: 7326-094

CURRENT APPLICATION NUMBER: US/09/270,767

CURRENT FILING DATE: 1999-03-17

NUMBER OF SEQ ID NOS: 62517

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 46823

LENGTH: 479
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Pred. No. 2.7;
0; Mismatches 4; Indels
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                                                                                                                                                                                                                                                                                                                           ; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-09-270-767-46823
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; ORGANISM: Drosophila melanogaster
US-09-270-767-58094
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Best Local Similarity 66.7%;
Matches 8; Conservative
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Best Local Similarity 66.7%;
Matches 8; Conservative
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RESULT 1
US-09-270-767-46823
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1 WSXWSXCSXXCG 12

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Gaps

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CITY: Columbia
STATE: Maryland
COUNTRY: USA
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US-09-270-767-42783
US-09-270-767-42783
Sequence 42783, Application US/09270767
Sequence 42783, Application US/09270767
Sequence 42781
GENERAL INFORMATION:
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster:
TITLE OF INVENTION Number: US/09/270,767
CURRENT PELING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 62517
SOFTWARE PATENTION VUMPER: US/09/270,767
SOFTWARE PATENTIAL VET. 2.0
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Sequence 7, Application US/09369364A

Patent No. 6391610

GENERAL INFORMATION:
APPLICANT: Apte, Suneel
APPLICANT: Hurskainen, Tiina L.
APPLICANT: Hirohata, Satoshi
TILLE OF INVENTION: Nucleic Acids Encoding Zinc Metalloproteases
FILLE REFERENCE: 264734607/10-30-00
CURRENT APPLICATION NUMBER: US/09/369,364A

CURRENT FILING DATE: 1999-08-06
NUMBER OF SEQ ID NOS: 31

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 7

LENGTH: 997
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Pred. No. 3.3;
0; Mismatches 4; Indels
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APPLICANT: Deutch, Alan Howard
APPLICANT: Deutch, George Paul
TITLE OF INVENTION: Peptide Fragments and Analogs of
TITLE OF INVENTION: Thrombospondin
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESSE:
ADDRESSEE: W. R. Grace & Co.-Conn.
STREET: 7379 Route 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-07-646-531D-6; Sequence 6, Application US/07646531D; Patent No. 5200397
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ORGANISM: Homo sapiens ADAMTS-7
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Best Local Similarity 66.7%;
Matches 8; Conservative
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Best Local Similarity 66.7
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         434 WSSWSDCSSKCG 445
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FILING DATE: 22-FEB-1990
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Best Local Similarity 66.7
Matches 8; Conservative
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Best Local Similarity
Matches 8; Conserv
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SEQ ID NO:6:
LENGTH: 23
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STATE: MI
COUNTRY:
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Sequence 12, Application US/09197770B

Patent No. 633962

GENERAL INFORMATION:
APPLICANT: Tuszynski, George

APPLICANT: Actor, Paul

TITLE OF INVENTION: THROMBOSPONDIN ACTIVITY

TITLE OF INVENTION: THROMBOSPONDIN ACTIVITY

FILE REFERENCE: 07206-0021

CURRENT PELIG DATE: 1998-11-23

NUMBER OF SEQ ID NOS: 38

SEQ ID NO 12

LENGTH: 23
                                                                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; OTHER INFORMATION: Description of Artificial Sequence: synthetic; ; OTHER INFORMATION: fragment/ analog of thrombospondin US-09-197-770B-12
                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                     DB 2; Length 23;
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5426100-6
; Patent No. 5426100
; Patent No. 5426100
; TITLE OF INVENTION: PIPTIDE FRAGMENTS AND ANALOGS OF
; TITROMBOSPONDIN
; VINBER OF SEQUENCES: 12
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/110,146
; FILING DATE: 20-AUG-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 896,527
; PLING DATE: 09-JUN-1992
; FILING DATE: 09-JUN-1992
; FILING DATE: 09-JUN-1992
                                  | REGISTRATION NUMBER: 36,317 | REPERENCE/OCKET NUMBER: 9598-2U4 | ELECOMOUNICATION: TELEPONE: (215) 567-2020 | TELEPAX: (215) 567-2991 | TELEPAX: 831-494 | TELEPAX: 831-494 | INFORMATION FOR SEQ ID NO: 6: SEQUENCE CHARACTERISTICS:
                 NAME: Leary Ph.D., Kathryn REGISTRATION NUMBER: 36,31
                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 66.7%;
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT
ORGANISM: Artificial Sequence
ATTORNEY/AGENT INFORMATION:
NAME: Leary Ph.D., Kathr
                                                                                                                                                                                       LENGTH: 23 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 66.7
                                                                                                                                                                                                                                                                                                                                                                                          1 WSXWSXCSXXCG 12
                                                                                                                                                                                                                                                                                                                                                                                                                             4 WSPWSSCSVTCG 15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4 WSPWSSCSVTCG 15
                                                                                                                                                                                                                                                       , MOLECULE TYPE: peptide
US-08-488-273-6
                                                                                                                                                                                                        amino acid
                                                                                                                                                                                                                                             linear
                                                                                                                                                                                                                      STRANDEDNESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 7
US-09-197-770B-12
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; Patent No. 1871969
; GENERAL INFORMATION:
    APPLICANT: HASTINGS, GREGG,
; APPLICANT: PATETCK J. DILLON
; TITLE OF INVENTION: HUMAN NEURONAL ATTACHMENT FACTOR-1
NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: HUMAN GENOME SCIENCES, INC.
; STREET: 9410 KEY WEST AVENUE
    6; Length 23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 55; DB 6; Length 23;
Pred. No. 0.24;
0; Mismatches 4; Indels
                                             4; Indels
                                                                                                                                                                                                             5426100-6
;Patent No. 5426100
;APPLICANT: DEUTCH, ALAN H.;TUSZYNSKI, GEORGE
; TITLE OF INVENTION: PIPTIDE FRAGMENTS AND ANALOGS OF
;. THROMBOSPONDIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Ploppy disk
COMPUTER: Ploppy disk
COMPUTER: Ploppy disk
COMPUTER: Ploppy disk
COMPUTER: ParentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/799,173A
FILING DATE: 11-FEB-1997
CLASSIFICATION: 536
ATTONEY/AGENT INFORMATION:
NAME: BROOKES, ANDERS A.
REGISTRATION NUMBER: 36,373
Score 55; DB 6, Pred. No. 0.24; 0; Mismatches
                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES: 12
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/110,146
FILING DATE: 20-AUG-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 896,527
                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE: 09-JUN-1992
APPLICATION NUMBER: 483,527
FILING DATE: 22-FEB-1990
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h 88.7%;
Similarity 66.7%;
8; Conservațive
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COUNTRY: USA
ZIP: 19103-2398
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
NAME: Appleby, Vanessa L.
REGISTRATION NUMBER: 33223
REFERENCE/DOCKET NUMBER: 01-7
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 531-4515
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 60 amino acids
TYPE: AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEX: 831-494
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                1 WSXWSXCSXXCG 12
                                                                                                                                                                                                                                                                                                                                                             7 WSPWSSCSVTCG 18
                                                                                                                                                                                   , MOLECULE TYPE: peptide US-07-646-531D-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: amino acid STRANDEDNESS:
                                                                                                                                                                        linear
                                                                                                                                                                      TOPOLOGY:
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Patent No. 5200397

GENERAL INFORMATION:
APPLICANT: Deutch, Alan Howard
APPLICANT: Tuszynski, George Paul
TITLE OF INVENTION: Thrombospondin
TITLE OF INVENTION: Thrombospondin
CORRESPONDENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: W. R. Grace & Co.-Con.
STREET: 7379 Route 32
                                                                                                                                                                                             Score 55; DB 2; Length 51;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 4; Length 51;
                                                                                                                                                                                                                                                                                                                                                             RESULT 11
US-09-170-042A-11

Sequence 11, Application US/09170042A

Patent No. 6759512

GENERAL INFORMATION:

APPLICANT: Hastings, Gregg

TITLE OF INVENTION: Human Neuronal Attachment Factor-1

PILE REPERRNCE: PF226D1

CURRENT APPLICATION NUMBER: US/09/170,042A

CURRENT FILING DATE: 1998-10-13

NUMBER OF SEQ ID NOS: 19

SEQ ID NO 11

LENGTH: 51

LENGTH: 51
                                                                                                                                                                                                                                    0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STATE: Maryland
COUNTRY: USA
ZIP: 21044
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 5.0
CURRENT APPLICATION DATA:
APPLICATION UNMER: US/07/646,531D
FILING DATE: 19910131
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           88.7%; Score 55; 66.7%; Pred. No. (
       TELEFAX: (301) 309-8512
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 51 amino acids
                                                                                                                                                                                           88.7%;
                                                                                                                                                                                             Query Match
Best Local Similarity 66.7
Matches 8; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6 WSEWSDCSVTCG 17
                                                                                TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECTLE TYPE: protein
US-08-799-173A-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity
Matches 8; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ALL...STREET: 75...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT
ORGANISM: rat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-07-646-531D-12
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Sequence 12, Application US/08488273
; Sequence 12, Application US/08488273
; Patent No. 5840692
; GENERAL INFORMATION:
   APPLICANT: Deutch, Alan H.
   APPLICANT: Deutch, George P.
   TITLE OF INVENTION: PEPTIDE FRACMENTS AND ANALOGS OF
   TITLE OF INVENTION: THROMBOSPONDIN
   NUMBER OF SEQUENCES: 15
   CORRESPONDENCE ADDRESS:
   ADDRESSEE: PANTICH SCHWARZE JACOBS & NADEL, P.C.
   STREET: 1601 Market Street, 36th Floor
   CITY: Philadelphia
   STATE: Pennsylvania
Score 55; DB 1; Length 60;
Pred. No. 0.52;
0; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OFFRAING STSTEM:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/488,273
FILING DATE: 07-JUN-1995
CLASSIFICATION NUMBER: US/08/488,273
FILING DATE: 07-JUN-1995
CLASSIFICATION NUMBER: US/08/488,273
FILING DATE: 19-DEC-1994
PRIOR APPLICATION NUMBER: US/08/110,146
FILING DATE: 20-AUG-1993
FILING DATE: 20-AUG-1992
FILING DATE: 30-AUN-1992
FILING DATE: 30-AUN-1992
FILING DATE: 32-FEB-1990
ATTCRNEY/AGENT INFORMATION: ACAILYN
REGISTRATION NUMBER: 36,317
REFERENCE/DOCKET NUMBER: 36,317
RELEPOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFRENK: (215) 567-2991
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0
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88.7%; Score 55; DB 2; Length 60;
Best Local Similarity 66.7%; Pred. No. 0.52;
Matches 8; Conservative 0; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          88.7%; Score 55; DB 6; Length 60; 66.7%; Pred. No. 0.52; tive 0; Mismatches 4; Indels
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5426100-12
FPACENT NO. 5426100
TITLE OF INVENTION: PIPTIDE FRAGMENTS AND ANALOGS OF
TITLE OF INVENTION NUMBER: US/08/110,146
FILING DATE: 20-0040-1993
FRIOR APPLICATION DATA:
APPLICATION NUMBER: 896,527
FILING DATE: 22-FEB-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          88.7%; Score 55; DB 6; Length 60; 66.7%; Pred. No. 0.52; tive 0; Mismatches 4; Indels
                                                                                                                                                                                                                                RESULT 14
5426100-12
; Patent No. 5426100
; Patent No. 5426100
; TITLE OF INVENTION: PIPTIDE FRAGMENTS AND ANALOGS OF
; THOMBOSPONDIN
; THOMBOSPONDIN
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/110,146
; FILING DATE: 20-AUG-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 896,527
; FILING DATE: 09-JUN-1992
; APPLICATION NUMBER: 483,527
; FILING DATE: 22-FEB-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 66.7
Matches 8; Conservative
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Best Local Similarity 66.7
Matches 8; Conservative
                                                                                                                                                1 WSXWSXCSXXCG 12
                                                                                                                                                                                  7 WSPWSSCSVTCG 18
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; TOPOLOGY: linear; MOLECULE TYPE: peptide US-08-488-273-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; LENGTH: 60
5426100-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQ ID NO:12:
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Search completed: April 1, 2005, 14:01:57 Job time : 22.1304 secs

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GenCore version 5.1.6 Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

April 1, 2005, 13:22:55 ; Search time 83.7391 Seconds (without alignments) 55.424 Million cell updates/sec Run on:

US-09-462-909D-7 62

1 WSXWSXCSXXCG 12 score: Sequence: BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

2105692 seqs, 386760381 residues Searched:

2105692 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

geneseqp2001s:*
geneseqp2002s:*
geneseqp2003as:*
geneseqp2003bs:* A Geneseq 16Dec04:* geneseqp19908:* geneseqp2000s:* . Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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g	Sea squir	Peptide	Human qen		Human gen	Human gen	Human gen	Amino ac	Drosophi	Human ADP	Human hea	Drosophi	ECMCAD pr	Mouse nov	Human BAI	Human sec	Human bra	Human nov	Drosophi]	Human 278	Human 278	Human ADA	Human ADA	Human met	Human ORF
Description	Adp04871	Aaw97445	Aae04264	Aae04262	Aae04263	Aae04268	Aae04266	Aab08135	Abb62815	Aab72283	Adj69288	Abb61710	Adi28031	Ado29008	Aaw99302	Aab23601	Abp81930	Ado29007	Abb66442	Aae00934	Aae00913	Aab74944	Adj58902	Aab86949	Aab41379
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QI	ADP04871	AAW97445	AAE04264	AAE04262	AAE04263	AAE04268	AAE04266	AAB08135	ABB62815	AAB72283	ADJ69288	ABB61710	AD128031	AD029008	AAW99302	AAB23601	ABP81930	AD029007	ABB66442	AAE00934	AAE00913	AAB74944	ADJ58902	AAB86949	AAB41379
DB	. 8	7	4	4	4	4	4	m	4	4	7	4	'n	æ	~	m	9	œ	4	4	4	4	ω	4	ო
% Query Match Length DB	324	12	27	100	149	189	191	206	763	997	997	1083	1255	1515	1522	1522	1522	1522	1682	1686	1686	1686	1686	1690	1784
% Query Match	91.9	90.3	90.3	90.3	90.3	90.3	90.3	90.3	90.3	90.3	90.3	90.3	90.3	90.3	90.3	90.3	90.3	90.3	90.3	90.3	90.3	90.3	90.3	90.3	90.3
Score	57	26	26	26	26	26	26	99	26	26	26	26	99	26	26	26	26	26	26	99	99	26	99	26	99
Result No.		7	m	4	Ω	9	7	80	σ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25

Abu62079 Human jel Adh48718 NOV1 prot Ab930203 Novel hum Adm59228 Human BEC Abg21064 Novel hum Aax13630 Fircmbosp Aaw81483 Thrombosp Aae20782 Alternati Adm80538 Thrombosp Add44504 Polypebti Aaw92465 Rat F-spo Add3574 Rat F-spo Adv3576 Human MET Aay49507 Human MET Aay49607 Human MET A	
ABU62079 ADH48718 ABG30203 ABG30203 AAR03528 AAR13630 AAR13630 AAR20782 AAR20782 AAR20782 AAR20785 AAR364995 AAR49504 AAX49507 AAX49507 AAX79507 AAX79062 AAG79061 AAB50009	
EQ170EEEE001111777770 CQ4740GC00700000044440	
4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4	
9900093339600333960003333960000333960000339600003396000033960000339600003396000033960000339600003396000033960000339600003396000033960000339600000300000000	
GGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG	

ALIGNMENTS

RESULT 1

Sea squirt protein with tissue specific expression in development Seq466. sea squirt; regeneration medicine; gene therapy; cell proliferation; differentiation; reproduction; environmental measurement; water survey. ADP04871 standard; protein; 324 AA. (first entry) Ciona intestinalis. 29-JUL-2004 ADP04871; ADP04871

JP2004057129-A.

26-FEB-2004.

31-JUL-2002; 2002JP-00222593.

31-JUL-2002; 2002JP-00222593.

(KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN.

WPI; 2004-287079/27. N-PSDB; ADP04870.

Novel gene cluster which is specifically expressed in tissue or organ during developmental phase of sea squirt, useful for elucidation of mechanism of development of tissue or organ of sea squirt.

Claim 1; SEQ ID NO 466; 1846pp; Japanese

This invention relates to novel genes and the encoded proteins thereof that are derived from the sea squirt Ciona intestinalis. Specifically, it refers to those genes that are expressed in the tissues or organs of the sea squirt during its developmental phase. The present invention describes the identification of these genes as useful for elucidation of the mechanism of development and hence for developing regeneration medicines and gene therapy techniques. Accordingly, they can be used in the research of various genetic diseases, as well as the analysis of cell proliferation, differentiation and reproduction. Furthermore, such compositions can be useful for senvironmental measurements and water surveys, particularly for sea water surveys, and also for the preparation of transformed sea squirt for improving edibility of sea squirt protein sequence that has tissue specific expression during development, given in

AAE04264 standard; peptide; 27 AA.

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The present sequence represents a peptide that stimulates neuronal (particularly axonal) sprouting in neurons of the cerebral cortex, and in spinal cord cells inhibits aggregation and defasiculation of neurites while increasing formation of synaptic contacts. The peptide is used to regenerate nervous system cells, particularly for treating neurodegeneration (e.g. Alzheimer's or Parkinson's diseases, multiple celevosis and myopathy), other conditions requiring regeneration (particularly elongation and synapse formation) or neuroblastoma. The peptide can also be used as an additive for neuronal cell cultures
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New polypeptides for promoting growth of neurons - useful for treatment of neurodegeneration, neuroblastoma and as additives for neuronal cell
                                                                                                                                                                                                                                                                                                                               Neuronal sprouting; cerebral cortex; spinal cord cell; aggregation; neurite defasiculation; regeneration; nervous system cell; nerodegenration; Alzheimer's; Parkinson's disease; multiple sclerosis; myopathy; synapse formation; neuroblastoma.
                                                                                  Gaps
                                                                                  ö
                                                                                                                                                                                                                                                                                                      Peptide that is useful for regenerating the nervous system.
                                                     Score 57; DB 8; Length 324; Pred. No. 2.9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 2; Length 12;
                                                                                  4; Indels
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66.7%; Pred. No. 0.25;
cive 0; Mismatches
                                                                                    0; Mismatches
an exemplification of the invention.
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                                                                                                                                                                                                                     AAW97445 standard; peptide; 12 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 6; Page 14; 29pp; French.
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                                                           91.9%;
66.7%;
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Query Match
Best Local Similarity 66.7
Matches 8; Conservative
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                                                                    Local Similarity 66.7
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                                                                                                                 1 WSXWSXCSXXCG 12
                                                                                                                                               85 WSSWSRCSSSCG 96
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                                Sequence 324 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                               WO9903890-A1
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AADOB488-AADOB529 represent cDNAs corresponding to 18 human secreted protein genes, and AAE04199-AAE04299 represent the proteins they encode. protein genes, and AAE04297 represent human secreted protein fragments or variants. The secreted proteins and their genes are useful for preventing, treating crow protein in a sample or by determining the amount of the pathological conditions can be diagnosed by determining the amount of the pathological conditions can be diagnosed by determining the amount of the converted in a sample or by determining the presence of mutations in new protein in a sample or by determining the presence of mutations in the new genes. Specific uses are described for each of the 18 genes, converted to the diagnosis or treatment of proliferative disorders (e.g., rheumatoid arthritis), inflammation, allergies, and include disorders (e.g., Alzhimer's disease, Parkinson's disease), cognitive disorders (e.g., Alzhimer's disease, Parkinson's disease), cognitive disorders, schizophrenia, asthma, skin disorders, cognitive disorders, schizophrenia, asthma, skin disorders, propagnic disorders, and also be used to aid wound healing and epithelial cell propagnic disorders, independent disorders, and infections. The propagnic tissues, to identify their cognate ligands or binding to reservative to modify storage properties. Antibodies specific for a preservative to modify storage properties. Antibodies specific for a preservative to modify storage properties. Antibodies specific for a preservation of the invention can be used as a food additive or preservation temperamental and be used in alleviating symptoms associated protein sequence represents and under above, and in diagnostic immunoassay or enzyme linked immunosorbent assay (ELISA). The radioimmunoassay or enzyme linked immunosorbent assay (ELISA). The preserve in the historian and human secreted protein fragment referred to heaven to historian and human secreted protein fragment referred to heaven to historian and human secreted protein fragmenting
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                                                                                                                                                                        Human; secreted protein; proliferative disorder; cancer; tumour; foetal abnormality; developmental abnormality; haematopoietic disorder; immune system disorder; AIDS; autoimmune disease; rheumatoid arthritis; inflammation, allergy; neurological disorder; Alzheimer's disease; parkinson's disease; cognitive disorder; schizophrenia; asthma; skin disorder; psoriasis; sepsis; diabetes; atherosclerosls; cardiovascular disorder; anglogenic disorder; kidney disorder; agastrointestinal disorder; pregnancy-related disorder; gene therapy; endocrine disorder; infection; wound healing; vulnerary; call culture; chemocraxis; food additive; binding partner identification; chromosome 7.
                                                                                                                               Human gene 8 encoded secreted protein fragment, SEQ ID NO:127.
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30-JUN-2000; 2000US-0215136P.
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                                                                                        09-AUG-2001 (first entry)
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AAD08488-AAD08529 represent cDNAs corresponding to 18 human secreted proteins genes, and AAE04199-AAB0423 represent the protein they encode. AAE04240-AAE04297 represent human secreted protein fragments or variants. The secreted proteins and their genes are useful for preventing, treating or ameliorating medical conditions, e.g., by protein or gene therapy. Pathological conditions can be diagnosed by determining the amount of the new protein in a sample or by determining the presence of mutations in the rissues in which they are most highly expressed, and include developing products for the diagnosis or treatment of proliferative developing products for the diagnosis or treatment of proliferative disorders, tumours, foetal and developmental abnormalities, disorders, diseases of the immune system, AIDS, autoimmune diseases (e.g., rheumatoid archritis), inflammation, allergies, neurological disorders (e.g., Alzheimer's disease, Parkinson's disease), cognitive disorders, disbetes, atheroselesis, cardiovascular disorders, angiogenic disorders, indorders, gastrointestinal disorders, angiogenic disorders, atheroselesis, cardiovascular disorders, propileration, to prevent skin ageing due to subburn, to maintain organs before transplantation, for supporting cell culture of primary tissues,
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   DB 4; Length 27;
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Score 56; DB 4
Pred. No. 0.5;
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                                                                                                                                                                                                                                                                                                                                                                                                         AAE04262 standard; protein; 100 AA.
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   90.3%;
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                           Best Local Similarity
Matches 8; Conserv
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   Query Match
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to regenerate tissues, to identify their cognate ligands or binding partners, and in chemotaxis, and can be used as a food additive or preservative to modify storage properties. Antibodies specific for a protein of the invention can be used in alleviating symptoms associated with the disorders mentioned above, and in diagnostic immunoassay or enzyme linked immunosorbent assay (BLISA). The present sequence represents a human secreted protein fragment referred to in the disclosure of the invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           foetal abnormality; developmental abnormality; haematopoietic disorder; inmune system disorder; AlDS; autoimmune disease; rheumatoid arthritis; inflammation; allergy; neurological disorder; Alzheimer; s disease; Parkinson's disease; cognitive disorder; schizophrenia; asthma; skin disorder; psoriasis; sepsis; diabetes; atherosclerosis; cardiovascular disorder; angiogenic disorder; kidney disorder; gastrointestinal disorder; pregnancy-related disorder; gene therapy; endocrine disorder; infection; wound healing; vulnerary; cell culture; chemotaxis; food additive; binding partner identification; chromosome 7.
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                                                                                                                                                                                 Score 56; DB 4; Length 100;
Pred. No. 1.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                secreted protein; proliferative disorder; cancer;
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                                                                                                                                                                                               Pred. No. 1.5;
0; Mismatches
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30-JUN-2000; 2000US-0215136P.
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Best Local Similarity 66...
8; Conservative
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AMENGAS29 represent cDNAB corresponding to 18 human secreted protein genes, and AAE04199-AAE04239 represent the proteins they encode.

Drotein genes, and AAE04199-AAE04239 represent the proteins they encode.

AAE04240-AAE04297 represent human secreted protein freagments or variants. The secreted proteins and their genes are useful for preventing, treating or ameliorating medical conditions. e.g., by protein or gene therapy.

CC reme protein in a sample or by determining the presence of mutations in the new genes. Specific uses are described for each of the 18 genes, based on the tissues in which they are most highly expressed, and include developing products for the diagnosis or treatment of proliferative disorders, tumnours, foetal and developmental abnormalities, haematopoietic disorders, diseases of the immune system, AIDS, autoimmune classactoric disorders, schizophrenia, asthma, skin disorders, e.g., Alzheimer's disease, Parkinson's disease), cognitive disorders, schizophrenia, asthma, skin disorders (e.g., Alzheimer's disorders, candioders, schizophrenia, asthma, skin disorders, engingenic disorders, sidney disorders, gastrointestinal disorders, pregnancy-related disorders, atherosclerosis, cardiovascular disorders, propingent of disorders, and meaning and epithalial cell properties and in chemotaxis, and can be used as a food additive or preters, and in chemotaxis, and can be used as a food additive or preters, and in chemotaxis, and can be used as a food additive or preservative to modify storage properties. Antibodies specific for a preservative to modify storage properties. Antibodies specific for a preservative to modify storage properties. Antibodies specific for a preservative to modify storage properties. Antibodies specific for a preservative to modify storage properties. Antibodies specific for a present sequence represents a human secreted protein fragment referred to redisorner of the invention
                                                                          Isolated nucleic acid molecule encoding a human secreted protein is used in preventing, treating or ameliorating a medical condition.
                                                                                                                                                                      Disclosure; Page 494-495; 509pp; English
                        WPI; 2001-343793/36.
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90.3%; Score 56; DB 4; Length 149; 66.7%; Pred. No. 2.1; ive 0; Mismatches 4; Indels Best Local Similarity 66.7 Matches 8; Conservative 1 WSXWSXCSXXCG 12 Sequence 149 AA; Query Match Matches ð

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Gaps ö

1 WSAWSSCSAPCG 12

AAE04268 standard; protein; 189 AA. 09-AUG-2001 AAE04268; AAE04268 RESULT

Human gene 8 encoded secreted protein fragment, SEQ ID NO:131.

(first entry)

Human; secreted protein; proliferative disorder; cancer; tumour; foetal abnormality; developmental abnormality; haematopoietic disorder; immune system disorder; AIDS; autoimmune disease; rheumatoid arthritis; inflammation; allergy; neurological disorder; Alzheimer's disease; parkinson's disease; cognitive disorder; schizophrenia; asthma; skin disorder; psoriasis; sepsis; diabetes; atherosclerosis; adisorder; anglogenic disorder; kidney disorder; gastrointestinal disorder; pregnancy-related disorder; gene therapy; endocrine disorder; infection; wound healing; vulnerary; cell culture; chemotaxis; food additive; binding partner identification; chromosome 7.

Homo sapiens

WO200136432-A2

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AMD08488-AAD08529 represent cDNA8 corresponding to 18 human secreted protein genes, and AAE04199-AAE04239 represent the protein they encode. Drotein genes, and AAE04199-AAE04239 represent the protein fragments or variants. The secreted protein or gene they encode. The secreted proteins and their genes are useful for preventing, treating or ameliorating medical conditions, e.g., by protein or gene therapy. Cor ameliorating medical conditions can be diagnosed by determining the amount of the new protein in a sample or by determining the presence of mutations in the new genes. Specific uses are described for each of the 18 genes, cancer, tumours, foetal and developmental abnormalities, discaders, cancer, tumours, foetal and developmental abnormalities, cancer, transuction arthritis), inflammation, allergies, autoimmune conditive disorders (e.g., Alzahimer's disease, Parkinson's disease), cognitive disorders, schizophrenia, asthma, skin disorders (e.g., Alzahimer's disease, Parkinson's disease), cognitive disorders, kidney disorders, atherosclerosis, cardiovascular disorders, angiogenic disorders, witherosclerosis, cardiovascular disorders, angiogenic disorders, witherosclerosis, cardiovascular disorders, preparancy-related disorders, atherosclerosis, cardiovascular disorders, proteins can also be used to and wound healing and epithelial cell colleration, to prevent skin againg due to sunburn, to maintain organs proliferation, to prevent skin againg due to sunburn, to maintain organs to reservative to modify storage properties Antibodies specific for a preservative to modify storage properties. Antibodies specific for a preservative to modify storage properties. Antibodies specific for a preservative to modify storage properties. Antibodies specific for a preservative to modify storage properties. Antibodies specific for a preservative to modify storage properties. Antibodies specific for a preservative to modify storage properties, and in diagnostic immunoassay or enzyme linked immunososy, and in diagnostic immuno
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                                                                                                                          19-NOV-1999; 99US-0166415P.
30-JUN-2000; 2000US-0215136P.
                                                                        15-NOV-2000; 2000WO-US031162.
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                         25-MAY-2001.
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Gaps ö Score 56; DB 4; Length 189; Pred. No. 2.5; 0; Mismatches 4; Indels 90.3%; ilarity 66.7%; Conservative Local Similarity ses 8; Conserv Sequence 189 AA; Query Match Best Loc Matches

in the disclosure of the invention

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RESULT 7

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AAE04266 standard; protein; 191 AA 09-AUG-2001 (first entry) AAE04266; AAE04266

Human; secreted protein; proliferative disorder; cancer; tumour; foetal abnormality; developmental abnormality; haematopoietic disorder; immune system disorder; AIDS; autoimmune disease; rheumatoid arthritis; Human gene 8 encoded secreted protein fragment, SEQ ID NO:129.

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AABO08489-AAD08529 represent cDNAs corresponding to 18 human secreted protein genes, and AAE04199-AAE04239 represent the protein they encode. AAE04240-AAE04297 represent human secreted protein fragments or variants. CT he secreted protein preventing, treating or ameliorating medical conditions, e.g., by protein or gene therapy. The secreted proteins can be diagnosed by determining the amount of the new protein in a sample or by determining the presence of mutations in can be diagnosed by determining the amount of the new protein in a sample or by determining the presence of mutations in the new genes. Specific uses are described for each of the 18 genes, can on the tissues in which they are most highly expressed, and include developing products for the diagnosis or treatment of proliferative disorders, tumours, foetal and developmental abnormalities, haematopoietic disorders, diseases of the immune system, AIDS, autoimmune disorders, cancer, tumours, foetal and developmental abnormalities, haematopoietic disorders (e.g., Alzahimer's disease, Parkinson's disease), cognitive disorders, schizophrenia, asthma, skin disorders (e.g., pregnancy-related disorders, and become disorders, and can disease, professions can also be used to aid wound healing and epithelial cell proliferation, to prevent skin ageing due to sunburn, to maintain organs before transplantation; for supporting cell culture of primary tissues, to regenerate tissues, to identify their cognate ligands or binding carriers, and in chemotaxis, and can be used as a food additive or protein of the invention can be used as a food additive or protein of the invention can be used in alleviating symptoms associated with the disorders mentioned above, and in diagnostic immunoassay or enzyme linked immunosociated protein fragment referred to repere the invention can be used in diagnostic immunoassay or enzyme linked immunosociated protein fragment referred to the historians.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Isolated nucleic acid molecule encoding a human secreted protein is used in preventing, treating or ameliorating a medical condition.
                  Parkinson's disease; cognitive disorder; schizophrenia; asthma; skin disorder; psoriasis; sepsis; diabetes; atherosclerosis; cardiovascular disorder; angiogenic disorder; kidney disorder; gastrointestinal disorder; pregnancy-related disorder; gene therapy; endocrine disorder; infection; wound healing; vulnerary; cell culture; chemotaxis; food additive; binding partner identification; chromosome?
  Inflammation; allergy; neurological disorder; Alzheimer's disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Komatsoulis GA, Baker KP, Young PE;
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Score 56; DB 4; Length 191; Pred. No. 2.5; 0; Mismatches 4; Indels 90.3%; Query Match Best Local Similarity Sequence 191 AA;

8; Conservative

Matches

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AAB08135 standard; protein; 206 AA.

AAB08135;

04-DEC-2000 (first entry)

Amino acid sequence of a KIAA0550 polypeptide

Type I repeat; thrombospondin-1; TSP-1; Type I repeat peptide; TRP; KIAA0688; KIAA0550; angiogenesis inhibitory protein; angiogenesis; cancer; tumour; rheumatoid arthrils; psoriasis; retinopathy; ocular angiogenic disease; mecular degeneration; corneal graft rejection; neovascular glaucoma; retrolental fibroplasia; rubeosis; osler-Webber Syndrome; myocardial angiogenesis; haemophiliac joint; plaque neovascularisation; telangiectasia; angiofibroma; wound granulation; coronary collateral; cerebral collateral; aretriovenous malformation; ischemic limb angiogenesis; neovascular glaucoma; retrolental fibroplasia; fracture; vasculogenesis; heliobacter related disease; hematopolesis; oyulation; menstruation; placentation; birth control; embryo implantation.

Homo sapiens.

WO200047622-A2.

17-AUG-2000

.5-FEB-2000; 2000WO-GB000520

99GB-00003408 15-FEB-1999; (OXFO-) OXFORD BIOMEDICA UK LTD.

Mazarakis N, Martin-Rendon E, Kingsman SM;

WPI; 2000-549137/50.

Non-naturally occurring Type I repeat peptide (TRP) derived from human thrombospondin-1, KIAA0688 or KIAA0550 proteins, useful in the treatment of angiogenesis and/or cancer.

Claim 5; Fig 7; 84pp; English.

specification describes a non-naturally occurring Type I repeat peptide (TRP), derived from human thrombospondin-1 (hTSP-1), KIAA0688 or KIAA0550 proteins. The From human thrombospondin-1 (hTSP-1), KIAA0688 or KIAA0550 proteins. The protein is an angiogenesis inhibitory protein. TRP proteins are used for the treatment of conditions associated with angiogenesis and cancer. Angiogenic mediated diseases include tumours, rheumatoid arthritis, pasoriasis, ocular angiogenic diseases, retinopathy of prematurity, macular degeneration, corneal graft rejection, neovascular glaucoma, retrolental fibroplasia, rubeosis), Osler Webber Syndrome, myocardial angiogenesis, plaque neovascularisation, telangiectasia, haemophiliac joints, angiofibroma, wound granulation, coronary collaterals, cerebral collaterals, arteriovenous malformations, ischemic limb angiogenesis, neovascular glaucoma, retrollental fibroplasia, heliobacter related diseases, fractures, vasculogenesis, hamatopoicesis, ovulation, menstruation and placentation. TRPs are also useful in the treatment of disease of excessive or abnormal stimulation of endothelial cells. TRP can also be used as a birth control agent, as it prevents the vascularisation required for embryo implantation The present sequence represents a KIAA0550 polypeptide. The

Sequence 206 AA;

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Gaps

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Gaps
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90.3%; Score 56; DB 3; Length 206; 66.7%; Pred. No. 2.7; 4; Indels ive 0; Mismatches 4; Indels
                                    8; Conservative
              Best Local Similarity
Matches 8; Conserv
   Query Match
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> RESULT 8 AAB08135

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This invention relates to multine and human ADAMTS-N (A disintegrin-like and metalloprotease domain with thrombospondin type I motifs) proteins, and metalloprotease domain with thrombospondin type I motifs) proteins, considerable and antibodies invention are cDNA sequences encoding the proteins, and antibodies invention are cords. The nucleic acid sequences and proteins may be specific for the proteins. The nucleic acid sequences and proteins may be using the nucleic acids, proteins and antibodies include, for example cusing the nucleic acids, proteins and antibodies include, for example tumour cachexia, inflammation, dermatosparaxis in cattle or Ehlers-Danlos tumour cachexia, inflammation, dermatosparaxis in cattle or Ehlers-Danlos in arthritic (EDS-VIIC) in humans, erosion of articular cartilage or in arthritic (both inflammatory and non-inflammatory) disease, and siscontrolling embryogenesis and implantation of fertilised eggs. The controlling embryogenesis and implantation of fertilised eggs. The present sequence represents human ADAMTS-7. The human ADAMTS-7 gene is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               mitochondrial; human; screening assay; diabetes mellitus;
Huntington's disease; osteoarthritis;
Leber's hereditary optic neuropathy; LHON;
mitochondrial encephalogathy lactic acidosis and stroke; MBLAS;
myoclonic epilepsy ragged red fibre syndrome; MBRRF; cancer;
neuroprotective; nootropic; antidiabetic; anticonvulsant; antiarthritic;
osteopathic; ophthalmological; cytostatic.
                                                                                                                                                                                                                                                                                                                                                                                                                            Murine and human 'A Disintegrin-like And Metalloprotease domain with ThromboSpondin type I motifs' proteins and the nucleic acids encoding them, useful for treating e.g. tumors, inflammation and arthritis.
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Pred. No. 10;
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                                                                                                                                                                                                                                                                                                                                  Hirohata S;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 15; Fig 4; 181pp; English
                                                                                                                                                                                                                             (CLEV-) CLEVELAND CLINIC FOUND
                                                                                                                                                                                     99US-00369364.
                                                                                                                                          03-AUG-2000; 2000WO-US021223.
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Best Local Similarity 66.7
Matches 8; Conservative
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                                                                                                                                                                                                                                                 APTE S S.
HURSKAINEN T L.
                                                                                                                                                                                                                                                                                                                                                                           WPI; 2001-159978/16.
                                                                                                                                                                                                                                                                                            HIROHATA S.
                                                                                                                                                                                                                                                                                                                                                                                                 N-PSDB; AAF63440.
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                                                        WO200111074-A2.
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                     Homo sapiens.
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                                                                                                       15-FEB-2001.
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(HURS/) /
(HIRO/) /
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention is useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL16175) and the encoded proteins (ABS57372-ABB72072). The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signaling and cell-cell interactions.
                                                                                                                                                                                                              Drosophila; developmental biology; cell signalling; insecticide;
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Pred. No. 8;
0; Mismatches 4; Indel8
                                                                                                                                                                      Drosophila melanogaster polypeptide SEQ ID NO 15237.
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                                                ABB62815 standard; protein; 763 AA.
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66.7%;
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11-JUL-2000; 2000US-00614150
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                                                                                                                                   (first entry)
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Best Local Similarity
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                                                                                                                                                                                                                                            pharmaceutical
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Venter JC, Adams M,
                                                                                                             2001-656860/75.
                                                     (PEKE ) PE CORP NY
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                                                                                                                        N-PSDB; ABL05813
                                                                                                                                                                                 interactions.
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Matches
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                                                                                                                                                                                                                                                                                                                                                          This invention relates to novel mitochondrial targets that can be used for therapeutic intervention in treating a disease associated with altered mitochondrial function. Specifically, it refers to a method for identifying proteins of the human heart mitochondrial proteome that are useful for drug screening assays, as well as therapeutic targets. The present invention describes a method for identifying such proteins that can be used in the treatment of various diseases associated with altered mitochondrial function including diabetes mellitus, Huntington's disease, osteoarthritis, Leber's hereditary optic neuropathy (LHON), mitochondrial encephalopathy lactic acidosis and stroke (MELAS), myoclonic epilepsy ragged red fibre syndrome (MERRF) or cancer. Accordingly, these
                                                                                                                                                                                                                                                       identifying a mitochondrial target for drug screening assays and for treating diseases associated with altered mitochondrial function, comprises detecting a modified polypeptide in a sample and correlating with the disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    compositions have neuroprotective, nootropic, antidiabetic, anticonvolsant, antiarthritic, osteopathic, ophthalmological and cytostatic activities. This polypeptide sequence is a human heart mitochondrial protein of the invention.
                                                                                                                                                                                             Glenn GM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Drosophila; developmental biology; cell signalling; insecticide;
pharmaceutical.
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Pred. No. 10;
0; Mismatches 4; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Drosophila melanogaster polypeptide SEQ ID NO 11922.
                                                                                                                                                                                                                                                                                                                                    Claim 1; SEQ ID NO 1094; 180pp; English.
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                                                                                          12-APR-2002; 2002US-0372843P.
17-JUN-2002; 2002US-0389987P.
20-SEP-2002; 2002US-0412418P.
                                                                 04-APR-2003; 2003WO-US010870.
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           WO2003087768-A2
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                                     23-OCT-2003
                                                                                                                                                                                           Ghosh SS, |
Warnock DE;
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A manuacturial paparotrophic; gene thereby:

W cytostatic; hepatotrophic; gene thereby:

W mann extracollular matrix and cell adhesion molecule; ECMCAD; diagnosis;

W mann extracollular matrix and cell adhesion molecule; ECMCAD; diagnosis;

W daucher's disease; myotonic dystrophy; bown's syndrome; cystic fibrosis;

W daucher's disease; myotonic dystrophy; sickle cell anemia; thalassemia;

W mins' tumor; immunological disorder; acquired immunodeficiency syndrome;

W mins' tumor; immunological disorder; acquired immunodeficiency syndrome;

W mins' tumor; immuno hemolytic anemia; contact dermatitis;

W atherosolerosis; autoimmune hemolytic anemia; contact dermatitis;

W doodpasture's syndrome; gout; Grave's disease; multiple sclerosis;

W systemic lupus erythematosus; ulcerative colitis; uvoitis;

W systemic lupus erythematosus; ulcerative colitis; uvoitis;

W meningical disorder; epilepsy; stroke; Alzheimer's disease;

W meningical disorder; parkinson's disease; multiple sclerosis;

W meningitis; periodic paralysis; mental disorder; moci, anxiety;

W schizophrenia; amnesia; disease; osteonecrosis; osteomyelitis;

Chondrosarcoma; giant cell tumor; psoriatic arthritis;

W minfectious arthritis; systemic sclerosis; cell proliferative disorder;

W actinic keratosis; atherosclerosis; cell proliferative disorder;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signaling and cell-cell
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                                                                                                                                                                                                                                        Myers EW;
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23-MAR-2000; 2000US-0191637P.
11-JUL-2000; 2000US-00614150.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 WSXWSXCSXXCG 12
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Tang YT, Yue H, Azimzai Y, He A, Batra S, Lo TP, Nguyen DB;
Burrill JD, Marcus GA, Zingler KA, Gandhi AR, Lal P, Kaarney L;
Burford N, Yao MG, Walia NK, Elliot VS, Patterson C, Khan FA;
Baughn MR, Hafalia AJA, Policky L, Au-Young J, Lu Y, Borowsky ML;
Lu DAM, Ramkumar J, Yang J, Gururajan R, Warren BA, Gietzen K;
Xu Y, Kallick DA, Lee EA, Thangavelu K, Delegeane AM, Lee S;
                                                                                                                                                                                                                                                                                                                                     Novel isolated human extracellular matrix and cell adhesion molecules
                                                                                                                                                                                                                                                                                                                                                 useful for treating, preventing connective tissue disorder e.g. osteoporosis, Paget's disease, genetic disorder e.g. cystic fibrosis,
adenocarcinoma; leukemia; lymphoma; melanoma; myeloma.
                                                                                                                                                                                                                                                                                                                                                                                            Claim 1; SEQ ID NO 23; 270pp; English.
                                                                                                                                            12-OCT-2000; 2000US-0240111P.
27-CCT-2000; 2000US-0244021P.
14-NOV-2000; 2000US-0249897P.
16-NOV-2000; 2000US-0249570P.
                                                                                                                                  12-OCT-2000; 2000US-0240106P
                                                                                       29-JUN-2001; 2001WO-US021067
                                                                                                                                                                                                     (INCY-) INCYTE GENOMICS INC.
                                                                                                                                                                                                                                                                                                     WPI; 2002-154732/20.
                                                                                                                                                                                                                                                                                                                  N-PSDB; ADI28067.
                                             WO200202634-A2.
                        Homo sapiens.
                                                                                                              30-JUN-2000;
                                                                                                                                                                                                                                                                                                                                                                        thalassemia
                                                                  10-JAN-2002
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The invention relates to a novel isolated human extracellular matrix and cell adhesion molecule (referred to as ECMCAD 1-36), its biologically cell adhesion molecule (referred to as ECMCAD 1-36), its biologically cell adhesion molecule is useful for screening a compound for ECMCAD 1-36. The molecule is useful for screening a compound for effectiveness as agonist or antagonist of itself. The protein and its encoding nucleic acid are useful in the diagnosis, treatment and prevention of genetic disorder such as adrenoleukodystrophy, Down's prevention of genetic disorder such as adrenoleukodystrophy, Down's syndrome, athalassemia, Milms' tumor, etc., immunological disorders such as acquired immunodeficiency syndrome, etc., immunological disorders such as acquired immunodeficiency syndrome, atharosclerosis, autoimmune hemolytic anemia, achma, atharosclerosis, autoimmune hemolytic anemia, contact dermatitis, Goodpasture's syndrome, gout, Grave's adisease, multiple sclerosis, osteoporosis, poriasis, rheumatoid arthritis, scleroderma, systemic lugus erythematosus, ulcerative colitis, uveitis, etc, a neurological disorder such as epilepsy, stroke, Alzheimmer's disease, Huntington's disease, Parkinson's disease, multiple sclerosis, batterial and viral meningitis, periodic paralysis, mental disorders including mood, anxiety, and schizophrenic disorders, mental disorders including mood, anxiety, and acell proliferative disorder such as actinic keratosis, atherosclerosis, bepatitis, psoriasis, cancers uch as actinic keratosis, atherosclerosis, hepatitis, psoriasis, cancers including adenocarcinoma, leukemia, lymphoma, melanoma, myeloma, etc.
This sequence represents one of the novel proteins.

Sequence 1255 AA;

90.3%; Score 56; DB 5; Length 1255; 66.7%; Pred. No. 12; 1; or 0; Mismatches 4; Indels Query Match
Query Match
Beet Local Similarity 66.79,
Bect Local Similarity 60.79, 113 WSAWSICSRSCG 124 1 WSXWSXCSXXCG 12

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ransgenic mouse; neurological disorder; adrenal gland disorder;

ransgenic mouse; neurological disorder; adrenal gland disorder;

colon disorder; intestinal disorder; adrenal gland disorder;

colon disorder; blood disorder; immune disorder; bone disorder;

yout disorder; metabolic disorder; nutritive disorder; cancer;

yout disorder; uterus disorder; prostate disorder; testis disorder;

skin disorder; tomach disorder; prostate disorder; selis disorder;

thymus disorder; thyroid disorder; nutritarklasonian; antimanic;

thymus disorder; thyroid disorder; nutianginal; antimarklythmic;

CMS; central nervous system; respiratory; antidiarrhoeic; antidiabetic;

virucide; hepatocropic; antibacterial; antianaemic; antidiabetic;

dermatological; antiulcer; antithyroid; antiallargic; anorectic;

minnosuppressive; nephrotropic; gene therapy; GPCR modulator; mouse; Gaitanaris GA, Bergmann JE, Gragerov A, Hohmann J, Li F; Madisen L, Mcilwain KL, Pavlova MN, Vassilatis D, Zeng H; Mouse novel GPCR BAI3, SEQ ID NO:107. AD029008 standard; protein; 1515 AA. 09-SEP-2003; 2003WO-US028226. 09-SEP-2002; 2002US-0409303P. (first entry) WPI; 2004-390329/36. (PRIM-) PRIMAL INC. N-PSDB; ADO29009 WO20040400000-A2 Mus musculus. 29-JUL-2004 13-MAY-2004 ADO29008; RESULT 14 ADO29008

Novel mammalian G protein coupled receptors, useful for identifying compounds that modulates diagnosing and treating disease condition associated with GPCR dysfunction e.g. autoimmune diseases, angina pectoris, Parkinson's disease.

Claim 1; SEQ ID NO 107; 542pp; English.

The invention relates to human and mouse G protein-coupled receptors (GPCRs) and nucleic acids encoding them. The invention also relates to sequences at least 90% identical to the GPCR proteins and nucleic acids of the invention, methods of treating, preventing or diagnosing diseases associated with GPCRs of the invention, methods of screening for compounds useful in the treatment of GPCR-related diseases, a transgenic compounds useful in the treatment of GPCR-related diseases, a transgenic mouse comprising a GPCR gene of the invention; a mouse comprising a mutation in a GPCR transgene or in an endogenous GPCR gene; cells derived from the transmagner mice; kits comprising several mice, each of which has a mutation in a different GPCR gene of the invention; and kits comprising probes which hybridise to GPCR polynucleotides of the invention. The probes which hybridise to GPCR polynucleotides of the invention. The used in the diagnosis, treatment or prevention of a wide variety of the used in the diagnosis, treatment or prevention of a wide variety of diseases including neurobathy, Parkinson's disease or schizophrenia); disorders of the adrenal gland; disorders of the colon or intestine of syndrome); cardiovascular disorders (e.g., angina, cardiac arrhythmia or myocardial infarction); muscular disorders; blood disorders (e.g.,

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AIDS); bone and joint disorders (e.g., osteoarthritis, rheumatoid arthritis, gout or osteoporosis); metabolic or nutritive disorders (e.g., obsestry, enzyme deficiency-related diseases or vitamin deficiency-related diseases); and disorders of the kidney, luver, lung, breast, ovary, uterus, prostate, testis, skin, stomach, pancreas, spleen, thymus and thyroid (e.g., cancers). The present sequence represents a GPCR of the invention. Note: The full sequence data for this patent did not form part of the printed specification; those sequences not shown were obtained in ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This sequence represents the human BAI3 protein. The gene is expressed specifically in the brain and plays an important role in cancer formation in the brain. The BAI3 protein can be used in drug compositions to diagnose, prevent or treat such cancers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New human BAI gene - is expressed in brain plays important role in cancer
 anaemia or leukaemia); immune disorders (e.g., autoimmune disorders or
                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human; BAI3; brain; cancer; drug; diagnosis; prevention; treatment.
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Pred. No. 14;
0; Mismatches 4; Indels
                                                                                                                                                                                                                                    90.3%; Score 56; DB 8; Length 1515; 66.7%; Pred. No. 14; ive 0; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                          AAW99302 standard; protein; 1522 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               97JP-00176485
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 97JP-00150460
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21-MAY-1999 (first entry)
                                                                                                                                                                                                                                                                                                                                     297 WSQWSACSVTCG 308
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Best Local Similarity 66.7
Matches 8; Conservative
                                                                                                                                                                                                                                    Query Match
Best Local Similarity 66.7
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                      1 WSXWSXCSXXCG 12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human BAI3 protein.
                                                                                                                                                                                                      Sequence 1515 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens
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AAW99302
ID AAW99:
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Search completed: April 1, 2005, 13:54:24 Job time : 86.7391 secs

297 WSQWSTCSVTCG 308

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